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Post-processing: Minimum Match 0%
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Perfect score:
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    protein search, using sw model
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length: 2000000000
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Sequence 2, Appli
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APPLICANT: Yue, Henry
APPLICANT: Corley, Meil C.
APPLICANT: Corley, Meil C.
APPLICANT: Corley, Meil C.
APPLICANT: Corley, Meil J.
APPLICANT: Corley, Meil J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: EXTRACEULULAR ADHESIVE PROTEINS
FILE REFERENCE: PF-0576 US
CURRENT APPLICATION NUMBER: US/09/131,648
CURRENT APPLICATION NUMBER: US/09/131,648
CURRENT FILMS DATE: 198-08-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
SEQ ID NO 2
LENGTH: 708
TYPE: PRF
ORGANISM: Homo sapiens
OTHER IMPORMATION: 2687731
US-09-131-648-2
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                                                                LEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLPELTKLD 316
                                                                                                                 GENPITRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPHVA
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Sequence 6, Appli
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TELEX: 610-407-0701

TELEX: 846169

INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-986-485-5
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US-08-986-485-5
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                                                                                                                                                            NAME: PRESTA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEPAN: 610-407-0701
TELEPAN: 610-407-0701
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNEE & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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APPLICANT: SWEET, RAXMOND
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 YVRNYLQKPTFALGELYPPLINLWEAGKEKSTSLKVKATVIGLPTN 706
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Best Local Similarity
Matches 169; Conserv
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GENERAL INFORMATION:
APPLICANT: WU, SHUJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 GLA-SLOELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEMLPNLEILMIG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 NSIVRYDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHLEENQLTRLEDHSFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 PSW--TRSLNLSYNRLSEIDSAAFEDLITNLQEVYLNSNELTAIPSLGTASIGVVSLFLQH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 RPWYTPRS---SYREATTYD------CNDLFLTAVPPALPA--GTQTLLLQS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 LAPRILLMILLILLQWPESAGAQARP-----RAPCAAACTCAGNSIDCSGRGLATLPRDL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRVTAEEAGLYTCVAQNLVG--ADTKTVSVVVGRALLQPGRDE----GQGLELRVQETHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNKYDAILDMNFRPLANLRSLYLAGMNLREISDYALEGLQSLESLSFYDNQLARVPR--- 254
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23.2%; Pred. No. 1.1e-31;
tive 106; Mismatches 255;
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MOLECULE TYPE: protein
US-08-986-485-2
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TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1101 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 21.8%; P. Matches 185; Conservative 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,485
FILING DATE: OB -DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REGERENCE/DOCKET NUMBER: 6H-7026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                    362 RSLRVLDLDHNEISGTIEDTSGAFSGLEFGH-SKLTLFGN-KIKSVAKRAFSGLEGLEHL 419
                                                                                                                                                                                                                                                                                                          249 LARVPRR-----
                                                                                                                                                                                                                                                                                                                                                      242 NSLEVIKLORNNISKITDGAFWGLSKMHVLHLEYDSLVEVNSGSLYGLTALHQIHLSNNS 301
                                                                                                                                                                                                                                                                                                                                                                                             189 PHLEILMIGGHKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 TRLEDHSFAGLA-SLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEML 188
                                         384 ----GTRVRFIEPQSTLC-----AEP-----
                                                                                                                                341 MLNNNALSALHQQTVESLPNLQEVGLHGNPIRCDCVIRW-----ANAT---- 383
                                                                                                                                                                                                                   285 LHLKELGLNNMEELVSID----KFALVNLPELTKLDITNNPRLSFIHPRAFHHLPOMETL 340
                                                                                                                                                                                                                                                                 302 IARIHRKGWSFCQKLHELVLSFNNLTRLDEESLAELSSLSVLRLSHNSISHIAEGAFKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                         183 GTLELGAFDGLSRSLLTLRLSKNRITQLÞVRAFK-LPRLTQLDLNRNRIRLIEGLTFQGL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 QVVALFLQQQQNRSLDGSQLKAYLSLEVLDLNLNNITEVRNTYFPHGPPIKELNLAGNRI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 LLLLWLLLLRLEPVTAAAGPRA-----PCAAACTCAGDPCTCAGDS-----LDCG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LLLAWV-----AGATATVEVVPWHVPCPPQCACQIREWYTPRSSYREATTVDCN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRGLAALPGDLPSWTRSLNLSYNKLAEIDPAGFEDLPNLQEVYLNNHELTAVASLGAGSS 122
                                                                                  NLGGNAIRSVQFDAFVKMKNLKELHISSDSFLCDCQLKWLPPWLIGRMLQAFVTATCAHP 479
ESLKGQSIFSVPPESFVCDDFLKPQIITQPETTMAMVGKDIRFTCSAASSSSSPMTFAWK 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 408; DB 3; Length 1101;
Pred. No. 1.5e-28;
44; Mismatches 277; Indels 264;
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
OS-08-190-802A-49
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                                                                                                                                                                                                        TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING TAPPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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STRET: F.C.
CITY: Palo Alto
CTATE: CA
CTATE: CA
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APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Dep
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          753
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                                                                                                                                                 TYPE: amino acid TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dehlinger & Associates STREET: P.O. Box 60850
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                                                                                                                                                                                          605 amino acids
                     Insulin-like growth factor binding protein complex, Fig. 32
                                                                                                                                                                                                                                   49:
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Query Match

10.9%; Score 407.5;

DB 1;

Length

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Sequence 49, Application US/OB477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Thereof
INUMBER OF SEQUENCES: 265
CORRESSOUNDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                            US-08-477-346-49
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Matches
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTIA Release #1.0, Version
CURRENT APPLICATION NUMBER: US/08/477,346
PILING DATE: 07-JUN-1995
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                                                                                                                                   COUNTRY: USA
ZIP: 20006-1812
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Best Local S
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ATTORNEY/AGENT INFORMATION:
NAME: MURASHIER, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 887-076
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
PTITING DATE: 07-JUN-1995
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Type: amino acid
TypoLovy: nob.

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                 DL 597
                                                                               NPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR
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                                              EV 411
                                                                                                              NPIRCDCVIR----WANATGTRV-RFIEP------QSTLCAEPPDLQRLPVR 409
                                                                                                                                                                                                               KD-NGLYGIEEQSLWGLAELLELDLISN-QLTHLPHRLEQGLGKLEYLLLSRNRLAELPA 475
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) 887-0763

TNO: 49:
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protein complex, Fig. 32
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RESULT 6
US-08-473-089-49
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 250-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELEPAN: (202) 887-0763
INFORMATION FOR SEO ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49,
                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: WD-40 - Derived Peptides
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
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APPLICANT: Ron, Dorit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: N
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                                                                                                                                               118
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                              3 LLVAPLILAMVA-----GATATVPVVPWHVPCPPQCACQIRPWYTPRSSY---REATT 52
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                                                                                                                                               LLGLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNL 177
                             FVQLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLSHNRVAGLLEDTFPGLLGLRVLRL
                                                        FEMLPNLEILMIGGNKVDAI------LDMN-----
                                                                                                              -----DHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRW 184
   -----FRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQLARV----
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2000 Pennsylvania Avenue,
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07-JUN-1995
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25.2%;
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Pred. No. 6.1e-29;
'2; Mismatches 173;
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NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 2
LENGTH: 673
TYPE: PRT
ORGANISM: Homo sapiens
US-09-063-950-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-063-950-2

; Sequence 2, Application US/09063950C

; Patent No. 6225085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.8%; Score 402; DB 4; Best Local Similarity 24.9%; Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/063,950C CURRENT FILING DATE: 1998-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: THEREFOR FILE REFERENCE: MEI-019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                           FYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDK 303
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VGLHGNPIRCDCVIRWAN--ATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREM-----
                                                                                                                    VSDNQLERVP----
                                                                                                                                                                                              ---RLPRLLLLDLSHNSLLA-LEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLD 222
                                                                                                                                                                                                                         WFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLS
                                                                                                                                                                                                                                                                                LTANRLHEITNETERGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLPLLLLLALG-----PGVQGCPSGCQCS----QPQTVFCTARQGTTV 46
                                                                                                                                                                                                                                                                                                                                                                PRDVPPDTVGLYVFENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLD
                                        ----GLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRL 292
                                                                            FALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPNLQE 363
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CURRENT APPLICATION NUMBER: US/09/063,950C
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 605
TYPE: PRT
ORGANISM: Papio hamadryas
US-09-063-950-5
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US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
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APPLICANT: HOLTZMAN, Douglas A.
TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MEI-019
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 150; Conservative
        209
                                    237 VFAQLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLSHNRVAGLLEDTFPGLLGLRVLR 296
                                                                             184 WFEMLPNLEILMIGGNKVDAI------LDMN----
                                                                                                                177 LGWNSLAVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKAN 236
                                                                                                                                                                  134
                                                                                                                                                                                              118 LLG-LENICHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLN 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        550 CGEAHTPPA---VHSNHAPVTQAREGNLPLLIA-PALAAVLLAA-LAAVGAAYCVRRG-- 602
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                                                                                                                                                                                                                                                                                                               53 VDCNDLFLTAVPPALPAGTQTLLLQSNSIVRV------
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                                                                                                                                                                                                                                                                                                                                                                                           3 LLVAPILLAWVA-----GATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREAT---T 52
                                                                                                                                       ------DHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSR 183
                                                                                                                                                                                                                               ELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHLEENQLTRLE------ 133
                                                                                                                                                                                                                                                                      LALALLLLSWVALGPRSLEGAEPGTPGEAEGPACPATCAC-----SYDDEVNELS 57
----FRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQLARV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%; Score 397.5; DB 4; Length 605; 24.9%; Pred. No. 5.1e-28; ative 73; Mismatches 173; Indels 207;
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	73 TLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHLEENQLTRL 132	y	
	18 LALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRNAE 64	9	
	VAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAVPPALPAGTQ:	, Q	
18	Query Match 9.5%; Score 355.5; DB 4; Length 1523; Best Local Similarity 21.8%; Pred. No. 1.8e-23; Matches 154; Conservative 94; Mismatches 259; Indels 199; Gaps	Quer Best Matcl	
	,	US-09-	
	LENGTH: 1523 TYPE: PRT ORGANISM: Homo sapiens	OR I	
	OFTWAKE: Patentin Ver. 2.1	SEQ	
	OR FILING DATE: 1998-08-13 BEER OF SEQ ID NOS: 5	NUM	
	PRIOR APPLICATION NUMBER: 60/096,420	; PRI	
	9	CUR	
	,	; TIT	
	PLICANT: Rajput, Bhanu True of Invention: Bhanu True of Invention: Human Slit Polypeptide and Polynucleotides Encoding	; APP ; TIT	
	SRAL INFORMATION: PLICANT: Connolly, Timothy	; GENE	
	uence 2, Application US/09182024A ent No. 6342370	; Sequ ; Pate	
	r 9 -182-024A-2	RESULT	
	595 RDL 597	DЪ	
	409 REV 411	Qy	
	535 GNPWDCSCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPVYTYNNITCASPPEVAGLDL 594	Ъ	
	368 GNPIRCDCVIRWANATGTRV-RFIEPQSTLCAEPPDLQRLPV 408	QУ	
	475 ADALGPLQRAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNNSLRTFTPQPPGLERLWLE 534	Db	
	351	Ωу	
	417 LKD-NGLVGIEEQSLWGLAELLELDLTSN-QLTHLPHQLFQGLGKLEYLLLSHNRLAELP 474	ф	
	292 LNNMEELVSIDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSAL- 350	Ωу	
		Db	
		Qy	
	297 LSHNAIASLRPRTFEDLHFLEELQLGHNRIRQLAERSFEGLGQLEVLTLDHNQLQEVKVG 356	망	

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US-08-190-802A-50
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                                                                                                   TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 50
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                       ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
 ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: WD-40 - Derived TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                     ANTI-SENSE:
                                                                  MOLECULE TYPE: protein
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Insulin-like growth factor bind
pro. complex-rat, Fig. 33
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RESULT 11
US-08-477-346-50
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Best Local Similarity 23.3
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                            Sequence 50, Application US/08477346 Patent No. 6262023
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                TITLE OF INVENTION: WD TITLE OF INVENTION: The NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415
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                                                                                      COUNTRY:
                                                                                                          STATE:
                                                                                                                                             ADDRESSEE: Morrison & Foerster STREET: 2000 Pennsylvania Avenue,
OPERATING SYSTEM:
                                                                        ZIP: 20006-1812
                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                      WD-40 - Derived Peptides and Uses Thereof
PC-DOS/MS-DOS
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Pred. No. 4.5e-23;
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Best Local 9
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/487,0
FILING DATE: 07-70W-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-JUN-
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                             188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LLLAWVA------GATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCN 56
                                                                                                                               EELVSIDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSAL-----
                                                                                                                                                                                               LFNVAVMNLSGNCLRSLPERVFQGLDKLHSLHLEHSCLGHVRLHTFAGLSGLRRLFLRD- 419
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CSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPANVSGLDLRDVSET
                                CDCVIR-----WANATGTRVRFIEP------QSTLCAEPPDLQRLPVREVPFR 414
                                                              GPLQRAFWLDISHNHLETLAEGLESSLGRVRYLSLRNNSLQTFSPQPGLERLWLDANPWD
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07-JUN-1995
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pro. complex-rat, Fig. 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score 344; DB 4; I
r; Pred. No. 4.5e-23;
63; Mismatches 194;
                                                                                                QTVESLPNLQEVGLHGNPIR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 603;
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                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 887-076 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknow MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                              92
                                                                                                                                                          62 SKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALLG- 120
                                                                                                                                                                                           57
                                                                                                                                                                                                                       13 LLAFWVALGPCHLQGTDPGASADAE----GPQCPVACTCS------HDDYTDELSVFCS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                       8 LLLAWVA------GATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCN 56
 LPNLEILMIGGNKVDAI - -
                               SLYVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVKANVFVH 240
                                                                                                                          LANLTELDLSQNSFSDARDCDFHALPQLLSLHLEENQLTRLE---
                                                                                                                                                                                         DLFLTAVPPALPAGTQTLLLQSNSIVRV------
                                                                                                                                                                                                                                                                                      141;
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                                                           -DHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEM 187
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2000 Pennsylvania Avenue,
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pro. complex-rat, Fig. 33
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Pred. No. 4.5e-23;
3; Mismatches 194
    -LDMN-
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16;

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GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/065,544
EEARLIER APPLICATION NUMBER: 60/081,057
EARLIER APPLICATION NUMBER: 60/081,057
EARLIER APPLICATION NUMBER: 60/081,057
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US-09-191-647-2
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SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 1525
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 126; Conserv
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                                         205
 195
                                                                           135 SENQIQAIPRKAFRGAVDIKNLQLDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVAS 194
                                                                                                                149 NHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEMLPNLEILMIGGNKVDAI----
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                                                                                                                                                      FAGLRHLRVLQLMENKISTIERGAFQDLKELERLRLNRNHLQLFPELLFLGTAKLYRLDL 134
                                                                                                                                                                                LGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHLEENQLTRLEDHSFAGLASLQELYL 148
                                                                                                                                                                                                                               CPAQCSC-----
                                                                                                                                                                                                                                                         CPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAVPPALPAGTQTLLLQSNSIVRVDQSE
FNHMPKLRTFRLHSNNLYCDCHLAWLSDWLRKRPRVGLYTQCMGPSHLRGHNVAEVQKRE 254
                                                                                                                                                                                                                                                                                                     8.9%; Score 331; DB 3; I arity 17.8%; Pred. No. 3.4e-21; Conservative 76; Mismatches 177;
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Qy Ov	Qy Db	Query Ma Best Loo Matches	RESULT US-09-54 Sequen Fatent GENERA APPLI APPLI APPLI APPLI TITLE FILE FILE FOURRE CURRE CURRE PRIOR	Qy Db	Qу	Qу	Qy	Дb	Qу	Qy	Qy Db	Db	Qy
89 LGYLANLTELDLSQNSFSDARDCUFHA               75 FAGLRHLRVLQLMENKISTIERGAFQD 149 NHNQLYRIAPRAFSGLSNLLRLHLNSN	9 CPPQCACQIRPWYTPRSSYR      :  8 CPAQCSC	atch 8.9%; Sc cal Similarity 17.8%; Pr 126; Conservative 76;	14 0-245A-2 0-245A-2 0-245A-2 No. 6270984 LINFORMATION: CANT: GOODMAN, COREY CANT: Kid, Thomas CANT: Tessier-Lavigne, Mar OF INVENTION: Modulating REPERENCE: B98-031-3 NT APPLICATION NUMBER: 09/0-03-31 NT FILING DATE: 1997-11-14 APPLICATION NUMBER: 60/08 FILING DATE: 1997-11-14 APPLICATION NUMBER: 60/08 FILING DATE: 1998-04-07 R OF SEQ ID NOS: 20 NO 2 TH: 1525 PRT TH: 1525 PRT 0-245A-2	84 GTRVREIEPOSTLCAEPPDLQRLPVREVPFREMT- :   :   :   :   :   :   :   :   :   :	348 SALHQQT	311 ELTKLDITNNP ;   : ; ;  555 QLRKINFSNNKITDIEEGAFEGASGVN	89	 35 PFICDCHLKWLADYLHTNPIETSGARC:	85LHLK	256ALEQVPGI   : : 375 LFSLQLLLLNANKINCLRVDAFQDLHNI	209FRPLANLRSLYLAGMNLRE	255 FVCSDEEEGHQSFMAPSCSVLHCPAACT	205
LGYLANITELDLSQNSESDARDCUFHALFQLLS III LEERQLIKKEEDHS RASLASLQELL 	CPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAVPPALPAGTQTLLLQSNSIVRVDQSE	ore 331; DB 4; Length 1525; ed. No. 3.4e-21; Mismatches 177; Indels 330;	45A C Robo: Ligand Interactions 19/540,245A 11,057	CAEPPDLQRLPVREVPFREMTDHCLPL 423   :   ::   ::   :         corpyflkeipiodvalodffcddgnddnscspl 720	SALHQQTVESLPNLQEVGLHGNPIRCDCVIRWANAT : : : : : : : : :   :           :   :	ELTKLDITUNP	ELGLNNMEELVSIDKFALVNLP 				FRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQLARVPRR 	EGHQSFMAPSCSVLHCPAACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEON	
1 140 1 134 - 204		Gaps 11			I 383 W 674	L 347 : I 614	P 310	3 494	288	- 284 V 434	374		208

Ъ	135	SENQIQAIPRKAFRGAVDIKNIQIDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVAS 194
Qy	205	204
Db	195	FNHMPKLRTFRLHSNNLYCDCHLAWLSDWLRKRPRVGLYTQCMGPSHLRGHNVAEVQKRE 254
Qy	205	
Db	255	FVCSDEEEGHQSFMAPSCSVLHCPAACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQN 314
		FRPLANLRSLYLAGMNLREISDYALEGLQSLESLSFYDNQLARVPRR 255
		PIKVIPPGAFSPYKKLRRIDLSNNQISELAPDAFQGLRSLNSLYLYGNKITELPKSLFEG 374
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Qy	289 -	ELGLNNMEELVSIDKFALVNLP 310
Db 4	95	DCFADLACPEKCRCEGTTVDCSNQKLNKIPEHIPQYTAELRLNNNEFTVLEATGIFKKLP 554
מט	555 (	QLRKINFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLESLKTLMLRSNRI 614
Qy	348 9	SALHQQTVESLPNLQEVGLHGNPIRCDCVIRWANAT 383
Ъ	615 1	TCVGNDSFIGLSSVRLLSLYDNQITTVAPGAFDTLHSLSTLNLLANPFNCNCYLAWLGEW 674
Qy 3 В 6	384 ( 675 I	GTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPL 423
RESULT 15 US-09-540-153; Sequence 2;	15 40-j	.53-2 2, Application US/09540153
GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT:	AL ICAN ICAN ICAN ICAN	
CURRE CURRE PRIOR PRIOR	ENT ENT ENT ENT ENT ENT R AP	NT APPLICATION NUMBER: US/09/540,153  NT FILING DATE: 2000-03-31  FAPPLICATION NUMBER: 09/191,647  FILING DATE: 1998-11-13  FAPPLICATION NUMBER: 60/081,057
SEQ I	NOMBER OF SI SOFTWARE: I SOFTWARE: I EQ ID NO 2 LENGTH: 15; TYPE: PRT ORGANISM: )	: PatentIn Ver. 2.0 2 1525 RT M: human
Query Match Best Local	C a	ch 8.9%; Score 331; DB 4; Length 1525; 1 Similarity 17.8%; Pred. No. 3.4e-21; 126. Concervative 76. Withhold 17. Table 20.
¥ ¥	29 C 28 C	QSE 88 ::: KTD 74
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ОУ	Qy Db	ОУ	ОУ	Qy Db	ОУ	Qy Db	ДУ	DЬ	Qy	ОУ	Qу
384 675	348 615	311 555	289 495	285 435	256 375	209 315	205 255	195	205	149 135	89 75
GTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPL 423 :   :   :   :   :   :   :   :	SALHQOT	ELTKLDITNNP	DCFADLACPEKCRCEGTTVDCSNQKLNKIPEHIPQYTAELRLNNNEFTVLEATGIFKKLP 554	288	284 LFSLOLLLLNANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAKGTFSDLRAIQTMHLAQN 434	FRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQLARVPRR 255	PVCSDEEEGHQSFMAPSCSVLHCPAACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQN 314	FNHMPKLRTFRLHSNNLYCDCHLAWLSDWLRKRPRVGLYTQCMGPSHLRGHNVAEVQKRE 254	204	NHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEMLPNLEILMIGGNKVDAI 204	LGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHLEENQLTRLEDHSFAGLASLQELYL 148
			J	W	45	- 51	w	#3	#>	** **	*- 00

Search completed: August 31, 2002, 14:35:27 Job time: 29 sec

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AAM79807 AAW410359 AAY02379 AAE03524 AAB93523 AAB93523 AAB94705 AAB74705 AAW4455 AAW4459 AAW13357 AAW12333 AAB060799 AAB060799 AAE060799 AAE06099 AAW1916910 AAW1916910

Human membrane ass Amino acid sequenc Amino acid sequenc Human PRO227 polyp Human PRO227 prote Human neuronal gui

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Polypeptide

AAY13355 AAY70030 AAM39309 AAU12320 AAB80223

AAY08100 AAW85722 AAY13394 AAB24407 AAY70673 AAU12355 AAU00826

Mature human neŭro Sequence used in d Murine glial cell Mouse LIG-1 protei Murine LIG-1 protei Human PRO331 protee Novel protein (Clo Amino acid sequenc Human PRO331 protee Human PRO331 protee Human PRO331 protee Human immune respo Human pRO331 prote Human prosi protein PRO331 protein PRO3

AAB80262 AAB65292

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Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;

Secreted protein; transmembrane protein; human; enterocolitis;

repair

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CAY13344-403 represent secreted and transmembrane human proteins.

The cDNA sequences are obtained from cDNA libraries, prepared from CR fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

The encoded polypeptides have specific uses based on their homology to CR known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the prepair of acute and chronic mucosal lesions

CR e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal CR clege enterocolitis, Zollinger-Ellison syndrome, gastrointestinal CR cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to CR content effects on cell growth and development, diseases related to CR content of the cylval of nerve cells including parkinson's disease, also be used as a creating content content
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RESULT 2
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ID AAB80253 standard; Protein; 713 AA.

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DE Human PRO293 protein.
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DE Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
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                                                                                                                                                                                                                                                                                The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 86; 393pp;
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ischaemia; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease)
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Filvaroff E,
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28-JUL-1999;
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                                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
les 713; Conservative (
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               sapiens.
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ki PJ, Grimaldi CJ, Gurney AL,
JP, Pan J, Paoni NF, Roy MA,
ms PM, Wood WI;
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ment of skin diseases (e.
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99WO-US28313.
99WO-US30095.
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99WO-US30999.
99WO-US00219.
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99WO-US21547.
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                                                                                                                                                           Score 3732;
Pred. No. 1e-
); Mismatches
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skin disease;
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Stewart TA,
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gastrointestinal disorder;
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n ME, Goddard ;
Kljavin IJ;
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                 Ota T,
Ishii
                                                                                                                                                                                                              Human protein
WPI; 2001-318749/34.
                                                                                                                                                                                             Human;
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                                                                                                                                                                                            primer;
               Isogai T,
Sugiyama
                                              HELIX RES INST.
                                                                                                                                                                                                                                                                     standard;
                                                              99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                (first entry)
                                                                                                                     2000EP-0116126
                                                                                                                                                                                                              sequence SEQ
                                                                                                                                                                                             detection; diagnosis; antisense therapy; gene
                  Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                     Protein;
                  hikawa T,
Wakamatsu
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                 Hayashi K,
A, Nagai K,
                            Saito
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC complementary to a CC polynucleotide which comprises as a sequence, where the CC complementary to a combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CC CNAB13633 to AAH13162 represent human cDNA sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 cof the present oligonucleotides, all of which are used in the exemplification.
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Best Local S
Matches 377
                                                                   AAB33472
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                                                                   standard;
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                                                                   Protein;
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12-APR-1999;
20-APR-1999;
                                             Ashkenazi AJ,
Kabakoff RC,
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13-SEP-1999;
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29-OCT-1999;
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15-SEP-1999;
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01-SEP-1999;
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02-JUN-1999;
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04-MAY-1999;
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26-JUL-1999;
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12-MAR-1999;
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                          J, Baker KP,
Lu Y, Pan
Tumas D, Wa
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antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; systemic sclerosis; sarcoidosis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; demyelinathing disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; inmunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease.
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GENENTECH
                                      99US-0134287

99US-0141037

99US-0144628

99US-0146222

99US-0146222

99US-0122011

99US-0122011

99WO-US2094

99WO-US21547

99WO-US21547

99WO-US21547

99WO-US28313

99WO-US28313

99WO-US28313

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99WO-US28313

99WO-US28313

99WO-US28551

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99WO-US30297

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antithyroid; antidiabetic; nootropic; neuroprotective;
hepatotropic; virucide; antipsoriatic; antiallergic;
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99US-0128849.
99WO-US08615.
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Pan J, Watanabe Goddard A, J, Pennica I tanabe CK, 1

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Hebert C, DL, Smith

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 335; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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N-PSDB; AAC58637.
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                                                        rvatikvngtll----dgtqvlkiyvkqteshsilvswkvnsnvmtsnlkwssatmkidn
                                                                                           KTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTWSSAS-SLRG
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53.6%;
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58; Pred. No. 3.5e-127;
104; Mismatches 166;
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The human PRO
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18-FEB-2000;

22-FEB-2000;

24-FEB-2000;

24-FEB-2000;

01-MAR-2000;

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01-MAR-2000;

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01-MAR-2000;

01-MAR-2000;

01-MAR-2000;
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02-JUN-2000;
10-NOV-2000;
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06-JAN-2000;
11-FEB-2000;
                                                       WPI; 200
N-PSDB;
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20-DEC-1999;
20-DEC-1999;
                                                                                              Gerritsen
                                                                                                      Baker
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01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                   02-DEC-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1999;
02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO1338 polypeptide sequence
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DB; AAS21499.
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Stewart
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                                                                                              Beresini M,
ME, Goddard
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                                                                                                                                          2000WO-US01376
2000WO-US01376
2000WO-US013565
2000WO-US04341
2000WO-US04341
2000WO-US04914
2000WO-US05601
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2000WO-US05601
2000WO-US07532
2000WO-US07532
2000WO-US013705
2000WO-US014042
2000WO-US14042
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Tumas
                                                                                 Deforge L, Desnoyers L, Filvaroff E, G
A, Godowski PJ, Gurney AL, Sherwood S;
Funas D, Watanabe CK, Wood WI, Zhang Z;
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Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                 626
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                                                                                                                            QGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEA---
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Best Local (
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Azimzai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences for 25 novel extracellular matrix and adhesion-associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-5, EXMAD-1, EXMAD-1, EXMAD-1, EXMAD-1, EXMAD-1, EXMAD-11, EXMAD-12, EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-18, EXMAD-19, EXMAD-20, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24 and EXMAD-25. They are useful in the prevention and treatment of cancers, cell proliferation, cardiovascular, reproductive, immune, musculoskeletal, developmental and gastrointestinal disorders and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polynucleotide encoding extracellular matrix or adhesion-associated protein (EXMAD) useful for diagnosing, treating, preventing disorders associated with expression of EXMAD such as proliferative, immune and genetic disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extracellular matrix and adhesion-associated protein; EXMAD;
inflammation; reproductive disorder; cardiovascular disorder;
immune disorder; musculoskeletal disorder; developmental disorder;
gastrointestinal disorder; cell proliferation disorder.
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23-AUG-1999;
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Pred. No. 3.5e-127;
4; Mismatches 166;
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The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
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RRSULT
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RAGG
                                                                                      The present sequence represents a human secreted polypeptide. The secreted polypeptides and polynucleotides are useful for treating contents and muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing metastasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, owary, prostate, remail gland, small intestine, heart, trachea, thymus, lymph node, muscular system and colon, for treating lipase deficiency in cystic fibrosis and pancreatitis, for treating undesirable clot formation contents and procedure sthat require decreased blood color formation, for treating procedures that require decreased blood color formation, for treating immune disorders, for treating inflammation and transplant crejection, for enhancing bone thickness and increasing bone density, for reducing the loss of essential ferroxidases, for suppressing the capptosis, and for regulating vascular smooth cell proliferation. They
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gastrointestinal ulceration; spinal cord disease; trachea disease;
thyroid gland disease; ovary disease; prostate disease; heart disea
renal gland disease; small intestine disease; thymus disease;
lymph node disease; muscular system disease; colon disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lipase deficiency; cystic fibrosis; pancreatitis; clot formation; myocardial infarction; angioplasty; liver disease; coagulation disorder; microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2001
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13-MAR-2000; 2000US-0188916
03-OCT-2000; 2000US-0236874
03-OCT-2000; 2000US-0237846
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N-PSDB; AAH78222.
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                                                                                                                                        Human polypeptide SEQ ID NO 3521.
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           WO200153312-A1
                                 Homo sapiens
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
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DB; AAI59532.
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KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithycoid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus crythematosus; infection;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation.
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                                                      Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
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Pred. No. 4.2e-124;
Pred. No. 4.2e-124; Indels 47;
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                           The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny/inhibin activity and may be useful in the diagnosis and/or activity/inhibin activity and may be useful in the diagnosis and/or
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N-PSDB; AAK51956.
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                                                                                                                               Sequence
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Wang D,
Yang Y,
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Wejhrman T,
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Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
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44.4%; Score 1656.5; DB 22
47.2%; Pred. No. 4.2e-124;
47.2%; Mismatches 217;
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                                                                                Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; flarkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
                          W09914328-A2
                                                                            anti-thrombotic;
                                                                                                                                                        Secreted protein;
                                                                                                                                                                                 Amino acid sequence of protein PRO220.
                                                                                                                                                                                                              25-JUN-1999
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Ţ Goddard A, Gurney ΑL, Pennica Ď Wood Ĭ, Yuan Ç.

N-PSDB; 1999-229533/19 DB; AAX52226.

gastrointestinal ulceration isolated human genes and polypeptides used in, e.g. treatment of

Fig 26; 320pp; English.

AAY13344-403 represent secreted and transmembrane human proteins. The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology taken not peptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions ţ

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anaemia; epilepsy; Cushing's syndrome; cell growth disorder; cell differentiation; embryogenesis; morphonementa. antiasthmatic; immunosuppressive; antiarteriosclerotic; distreatment; prevention; cancer; leukaemia; melanoma; immune rheumatoid arthritis; asthma; atherosclerosis; developments tein; EXADH2; cytostatic; antiart antiarteriosclerotic; diagnosis; disorder; antiarthritic;

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Location/Qualifiers

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The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with abnormal expression of EXADH particularly cancers such as leukaemia and melanoma, immune disorders such as fewer and and theorosclerosis, and developmental disorders such as anaemia, epilepsy, Cushing's syndrome and any disorder associated with cell growth, differentiation, embryogenesis and associated with cell growth, differentiation, embryogenesis and
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                                                         Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
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Wehrman T,
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WPI; 2001-442253/47. N-PSDB; AAI58465.

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02-DEC-1999;
09-DEC-1999;
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24-FEB-2000;
01-MAR-2000;
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21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                        Gerritsen Smith V,
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                                                                                          Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                           02-JUN-2000;
10-NOV-2000;
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11-FEB-2000;
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N-PSDB; AAS21392.
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30-MAY-2000;
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22-FEB-2000;
AAU12172-AAU12446 represent novel human PRO polypeptides. The PRO polypeptides arepsilon
                                                             Claim 12;
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Stewart
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ME, Goddard
Stewart TA,
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2000WO-US00277.
2000WO-US00375.
2000WO-US03555.
2000WO-US04341.
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CC PRO polypeptides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC Some of the 275 sequences are also useful to stimulate the release of CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or CC gene expression in pericyte cells, the release of proteoglycans from CC artilage, the proliferation of inner ear utricular supporting cells or CC of T-lymphocytes, the release of a cytokine from peripheral blood CC monocytes (PBMCS), or the proliferation of endothelial cells. Some of CC the PRO polypeptides may modulate glucose or free fatty acid uptake by Skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC to factor VIIA. The PRO polypeptides can be used in assays to identify CC molecules involved in binding interactions. The polymucleotides encoding CC PRO polypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 44.4%; Score 1656.5; DB 22; Lengt Best Local Similarity 47.2%; Pred. No. 4.3e-124; Matches 333; Conservative 109; Mismatches 217; Indels
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yvrnylqkptfalgelypplinlweagkekstslkvkatviglptn 706
                                                                                                                        glhpdqkeyeknntttlmaclggllgiigviclisc!
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                                                                                                                                                                                      ----EATSCHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVGGRR- 663
                                                          -----PLPPAWAFWGWSAPSVRVVSAPLVLPWN 691
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> Search completed: August 31, Job time: 71 sec 2002, 14:36:09

1     1649.5     44.2     707     2     JC7763       2     442.5     11.8     10.9     605     2     A41915       3     407.5     10.9     605     2     A41915       3     407.5     10.9     605     2     A41915       3     30.5     10.2     7082     2     T28717       6     381.5     10.2     1355     2     T28715       7     368     9.9     907     2     T27218       8     360.5     9.7     1531     2     T42218       9     360     9.6     907     2     JE0176       10     346     9.3     1523     2     T13953       11     344     9.2     603     2     JC1282       12     342.5     9.2     603     2     JC1282       14     324     8.7     1469     2     A3665       14     324     8.7     1469     2     A36665       14     324     8.7     1469     2     A36665       18     299.5     8.1     1025     2     T21148       19     299.5     8.0     536     2     T13860 <t< th=""><th>Result Query NO. Score Match Length DB ID</th><th>icted k e of th score</th><th>Database : PIR_71:*  1: Pir1:* 2: Pir2:* 3: Pir3:* 4: Pir4:*</th><th>Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</th><th>Minimum DB seq length: 0 Maximum DB seq length: 2000000000</th><th>otal number of hits satisfying chosen parameters: 2</th><th>Gapop 10.0 , Gapext 0.5</th><th>PLLLAWVAGATATV</th><th>August 31, 2002, 14:34:58; Search ti (without 2813.622</th><th>OM protein - protein search, using sw model</th><th>GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd</th></t<>	Result Query NO. Score Match Length DB ID	icted k e of th score	Database : PIR_71:*  1: Pir1:* 2: Pir2:* 3: Pir3:* 4: Pir4:*	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	otal number of hits satisfying chosen parameters: 2	Gapop 10.0 , Gapext 0.5	PLLLAWVAGATATV	August 31, 2002, 14:34:58; Search ti (without 2813.622	OM protein - protein search, using sw model	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
SSMILARITY 47.5%; Pred. N SSMILARITY 47.5%; Pred. N 7; CONSETVATIVE 112; MISH 77; CONSETVATIVE 112; MISH QIHVLIGLAITALVQAGDKKVDCPQLGT QIHVLLGLAITALVQAGDKKVDCPQLGT LPAGTQTLLLQSNSIVRVDQSELGYLAN LPADTQILLLQTNNIARIEHS-TDFPVN NQLTRLEDHSFAGLASLQELYLNHNQLY	rr-3 3: cell adhesion 44.2%:	AF291437 , a new member of the raction and functions	A; Title: Rat neuronal leucine-rich repeat protein-3: Cloning and A; Reference number: JC7763; PMID:11549284 A; Contents: Fibrosarcoma cells A; Accession: JC7763 A; Accession: JC7763	C; species: kattus norvegicus (Norway rat) C; bate: 01-reb-2002 #sequence_revision 01-reb-2002 #text_change C; Accession: JC7763 C; Kitanaka, C; Kuchino, Y; Tsuda,	JC7763 neuronal leucine-rich repeat protein-3 - rat	83138	AT. TONMENTS	262.5 7.0 1051 2 261 7.0 359 1 261 7.0 360 2 258 6.9 354 2	me 24.35 Seconds 37 268 7.2 360 2 S06280 alignments) 38 266 7.1 1097 2 A29943 Million cell updates/sec 40 263 7.0 1535 2 S46224 40 263 7.0 1016 2 T30553 41 262 5 7.0 562 2 T34319	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	30 280.5 7.5 662 2 31 276.5 7.4 357 2 32 274.5 7.4 575 2 33 273 7.3 1112 2
AD C. 4.56-105;  AD CO. 4.56-105;  AD COIRPWYTPRSSYREATTYDCNDLFLTAV 63	DB 2; Length 707;	neuronal leucine-rich repeat protein fam as a cell adhesion molecule or soluble l	-3: Cloning and regulation of the ge	2 #text_change 01-Feb-2002 ino, Y.; Tsuda, H.				gp150 protein - fr decorin precursor decorin - rabbit decorin precursor		chaoptin precursor oncofetal trophobl decorin precursor	<pre>garp precursor - h decorin precursor hypothetical prote disease resistance</pre>

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363

ISIHSNPIRCDCVIRWINMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPL

422

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A58332

A58332

A58332

A58332

Glial cell membrane glycoprotein LIG-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
C;Accession: A58332

R;Suzuki, Y; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
J. Biol. Chem. 271, 22527-22527, 1996
A;Title: cDNA cloning of a novel membrane glycoprotein that is expressed specif
A;Title: cDNA cloning of a novel membrane glycoprotein that is expressed specif
A;Reference number: A58532; MUID:96394313
A;Accession: A58532; MUID:96394313
A;Accession: A58532; MUID:96394313
A;Accession: A58532; MUID:96394313
A;Accession: A58532; MUID:96394313
A;Cross-references: GB:D78572; NID:g1545806; PIDN:BAA11416.1; PID:g1545807
A;Cross-references: GB:D78572; NI
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Best Local Similarity
                    127
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                                                                                                                                                                                                                                                   RPWYTPRS---SYREATTVD-----
                                                                                                                                                                                                                                                                                                                       LAPRILLWLLLLLLQWPESAGAQARP----RAPCAAACTCAGNSLDCSGRGLATLPRDL
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                                                                                                                                                                  PSW--TRSLNLSYNRLSEIDSAAFEDLTNLQEVYLNSNELTAIPSLGTASIGVVSLFLQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 442; DB 2;
%; Pred. No. 4.8e-22;
106; Mismatches 255
                                                                                                                                                                                                                                          -CNDLFLTAVPPALPA - -GTQTLLLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1091;
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F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homológy <LRR3>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6-
F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6-
F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7-
F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8-
F:219-242-Z66/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9-
F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9-
F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10-
F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10-
F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: mRNA; protein
A; Residues: 1-605 < LEO>
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A; Title: Structure and functional expression
A; Reference number: A41915; MUID:92357025
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R;Leong, S.R.; Baxter, R.C.; Camerato, T.;
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insulin-like growth factor acid-labile chain - bal C:Species: Papio sp. (baboon)
C:Date: 17-Apr-1997 #sequence_revision 09-May-1997
C:Accession: JC5239
R:Delhanty, P.; Baxter, R.C.
Biochem. Blophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon A:Reference number: JC5239; MUID:97040714
A:Contents: liver
A:Accession: JC5239
A:Molecule type: mRNA
A:Residues: 1-605 < DELY
C:Comment: This factor is structurally related to
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F;387-410/Domain: 1
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2; Mismatches 173;
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A; Molecule type: DNA
A; Residues: 1-789 < MODE
A; Residues: 1-789 < MODE
A; Cross-references: EMBL: AF016687; PIDN: AAC48096.1; GSI
A; Experimental source: strain Bristol N2; clone T21D12
A; Experimental source: strain Bristol N2; clone T21D12
A; Gene: CESP:T21D12.9a
A; Map position: 4
A; Introns: 38/2; 84/2; 132/2; 204/2; 275/2; 351/2; 519,
                                                                                                                             A; Reference number: Z20514
A; Accession: T28714
A; Status
                                                                                                                                                                                                                    hypothetical protein T21D12.9a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex C;Accession: T28714
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                                                                                                                                                                        submitted to the EMBL Data Library, August A; Description: The sequence of C. elegans
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Pred. No. 2.
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     615/1;
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                                                                                                                                                                                                                                                                      hypothetical protein T21D12.9b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28715
R;Woessner, J.
R;Woessner, J.
A;Description: The EMBL Data Library, August 1997
A;Description: The sequence of C. elegans cosmid T21D12.
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1355 <WOE>
A;Residues: 1-1355 <WOE>
A;Cross-references: EMBL:AF016687; PIDN:AAC48095.1; GSPDB:GN00022; CESP:T21D12.
A;Experimental source: strain Bristol N2; clone T21D12
C;Genetics:
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A; Introns: 38/2;
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Local Similarity 24.0 nes 144; Conservative
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144; Conserv
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Pred. No. 4.2e-18
81; Mismatches 2:
                                            ; Score 381.5; DB 2;
; Pred. No. 9.2e-18;
81; Mismatches 215;
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2e-18;
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c;Species: Mus musculus (house mouse)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0193
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A; Residues: 1-907 <HE
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301 IDKFALVNLPELTKLDITNNP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLDLSYNQIQSFHISSWSHTPKLKWLSLHSNRIQSLPSGSFRVLRQLEELIL-SANSIDS
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                                                                                    YQCVARNRFGSDFSTHVKLQVYQAPKFTYTPEDMPLLVGQTAKFLCAATGTPRPEIKWAF
                                                                                                                                                                                                                                                                             SIIAKCSYPPPLADLYVVAIDTANLTCHNDSPRAKIVRQPVEVSTLIGEKARFTCNVYGA
                                                                                                                                                                                                                                                                                                                                                                    FPALEELDLTDNPIATIHPEAFEPL-ELKRLVMNSSSILCDCQISWLASWIYRLK-LDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHKFALVGMSSLHKLDLSSNTLAVCVEDGAVLYNTSMPFLRSLRFTNNQLRVIPKRAFER
EQIP-----FPAAEARRLYVTPNDDHIYIMNVTKEDQGAYTCHATNVAGQTQASANLIV 613
                                      --TPAGLRLTPAHAGRRYRVYP-EGTLELRRVTAEEAGLYTCVAQNLVGADTKTVSVVV
                                                                                                                                                                                 SPLSIEWRVMENGQPRVLVQDSATFLSINRTAVVNGTFDERELAAAELLLDNVAMTDNSE
                                                                                                                                            LPLISPRSF---PPSLQVASGESMVLHCRALAEPEPEIYWV-
                                                                                                                                                                                                                                        -----REVPFRE-----MTDH--
                                                                                                                                                                                                                                                                                                                                     -RLPV----
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R;Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I. Blochem. Blophys. Res. Commun. 254, 273-279, 1999
A;Title: Identification of a novel seven-transmembrane receptor with. A;Reference number: JG0193; MUID:99121227
A;Accession: JG0193
A;Status: preliminary Query Match Best Local Similarity Matches 116; Conserv TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL 120 DSRWFEMLPHLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE VLMLQNNQLRKVPEEALQNLRSLQSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTDV SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI SELPSNLSVFTSYLDLSMNNISOLPASLLHRLCFLEELRLAGNALTHIPKGAFTGLHSLK 117 MLLSLLALLQLVAAGSSPGPDAIP--RGCPSHCHCEL-----DGRMLLRVDCSDLGL MRLLVAPLLLAWVAGATATVPVVVWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL 9.9%; ilarity 29.6%; Conservative 5 ; Score 368; DB 2; ; Pred. No. 4.3e-17; 59; Mismatches 157 157; Length 907 Indels 60; homology Gaps 177 180 240 57 8 6 glyc

the gl

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RESULT 8
T42218
T42218
Slit-1 protein homolog - rat
N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T42218
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like
A;Reference number: Z14126; MUID:98360089
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRMA
A;Residues: 1-1531 <NAK>
A;Cross-references: EMBL:AB011530; NID:g3449289; pIDN:BAA32460.1; PID:g3449290
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLL---AWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAVP 64
      LCAEPPDLQRLPVREVPFREM---
                                                                                                                      AEIAPDAFQGLRSLNSLVLYGNKITDLPRGVFGGLYTLQLLLLNANKINCIRPDAFQDLQ
                                                                                                                                                                                                                                                                                        GLFTQCSGPASLRGLNVAEVQKSEFSCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRNQLQVLPELLFQNNQALSRLDLSENSLQAVPRKAFRGATDLKNLQLDKNQISCIEEGA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRW 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESLTLTGAKISSLPQAVCDQLPNLQVLDLSYN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNA----
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                                          NLSLLSLYDNKIQSLAKGTFTSLRAIQTLHLAQNPFICDCNLKWL-ADFLRTNPIETTGA
                                                                                QMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQST
                                                                                                                                                                  VSIDKFALVNLPELTKL----DITNNPR----
                                                                                                                                                                                                      SCSNGIVDCRGKGLTAIPANLPETMTEIRLELNGIKSIPPGAFSPYRKLRRIDLSN-NQI
                                                                                                                                                                                                                                                                                                                                                                    FRALRGLEVLTLNNNNITTIPVSSFNHMPKLRTFRLHSNHLFCDCHLAWLSQWLRQRPTI
                                                                                                                                                                                                                                                                                                                                                                                                              FEMLPNLEILMIGGNKVDAILDMNFRPLANLRSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNIPRNTERLELNGNNITRIHKNDFAGLKQLRVLQLMENQIGAVERGAFDDMKELERLRL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLWAAAWRLGATA------CPALCTC-----TGTTVDCHGTGLQAIP 56
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                                                                                                                                                                                                                                                                                                                            -VLAGMNLREI--SDYALEGLQSLESLSFYDNQLARVPR------
                                                                                                                                                                                                                                              -RALEQVPG-----LKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 360.5; DB 2; Length 1531; Pred. No. 3e-16; Mismatches 216; Indels 149;
  -TDHCLPLISPRSFPPSLQVASGESMVLHCRALAE
                                                                                                                                                                                                                                                                                      -QGEAAQVPACTLSSGSCPAMC
                                                                                                                                                                ------LSFIHPRAFHHLP
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A; Map Position: 12q22-23
A; Map Position: 12q22-23
F; 1-21/Domain: signal sequence #status predicted <TM1>F; 562-583/Domain: transmembrane #status predicted <TM2>F; 594-616/Domain: transmembrane #status predicted <TM2>F; 639-660/Domain: transmembrane #status predicted <TM4>F; 639-660/Domain: transmembrane #status predicted <TM4>F; 681-701/Domain: transmembrane #status predicted <TM5>F; 725-744/Domain: transmembrane #status predicted <TM5>F; 7764-791/Domain: transmembrane #status predicted <TM7>
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A;Cross-references: GB:AF062006; NID:g3366801; PIDN:AAC28019.1; PID:g3366802
A;Crosmment: This protein is a receptor for a novel class of glycoprotein ligar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orphan G protein-coupled receptor precursor - human C;Species: Homo sapiens (man) C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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C;Genetics:
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Best Local Similarity
Matches 134; Conserv
457
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                                                                              AEPPDLQRLPVREVPFREM-TDHCLPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIY
                                                                                                                        LTLTGAQISSLPQTVCNQLPNLQVLDLSYN
                                                                                                                                                                                                      EKAFVGNPSLITIHFYDNP-IQFVGRSAFQHLPELRTLTLNGASQITEFPDLTGTANLES
                                                                                                                                                                                                                                                                                                                          SFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSID
                                                                                                                                                                                                                                                                                                                                                                                                          RWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSL 122
                                                                                                                                                            -----LSALHQQTVESLPNLQEVGLHGNPIRCDCVIRWANATGTRVRFIE---POSTLC
                                                                                                                                                                                                                                                                                    HLHNNRTHSLGKKCFDGLHSLETLDLNYNNLDEF-PTAIRTLSNLKELGFHS-NNIRSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLQNNQLRHVPTEALQNLRSLQSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPSNLSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLSLPVLLQLATGGSSPRSGVLLR-GCPTHCHCE-----PDGRMLLRVDCSDLGLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPEIYWVTPAGLRLT---PAHAGRRYRVYPEGTLELR 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCASPRRIANKRIGQIKSKKFRCSAKEQYFIP--GTEDYHLNSECTSDVACPHKCRC---
                                     LQKIDLRHNEIYEIKVDTFQQLLSLR----SLNLAWNKIAIIH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                  -----PVQA-----FRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%; Pre
27.4%; Pre
70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 360; DB 2;
Pred. No. 1.5e-16;
0; Mismatches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen, F.;
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                                                                                                                      LEDLPSFSVC
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                                          418
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N:Alternate names: slit protein homolog C:Species: Rattus norregicus (Norway rat) C:Date: 20-Sep-1999 #sequence_revision 20:C:Accession: T13953 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Genomics 51, 27-34, 1998
insulin-like growth factor-bi
C; Species: Rattus norvegicus
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A; Gene: MEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1523 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126; MUID:98360089 A;Accession: T13953 A;Accession: T13953 A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                          JC1282
                                                           RESULT
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Best Local Sim
Matches 132;
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                                                                                                                   -EGTIVDCSNQKLSRIPSH-
                                                                                                                                                    PEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELR 485
                                                                                                                                                                                          ANKRISQIKSKKFRCSGSEDYRNRFSSECFMDLVCPEK-
                                                                                                                                                                                                                                                                                                    NNALSALHQQTVESLPNLQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDL 403
                                                                                                                                                                                                                                                                                                                                                                            MLHLKELGLNNMEELVSIDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLN 343
                                                                                                                                                                                                                                                                                                                                                                                                            RGKGLTEIPANLPEGIVEIRLEQNSIKSIPAGAFIQYKKLKRIDISKNQISDIAPDAFQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGAFRALRDLEILTLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRLNKNKLQVLPELLFQSTPKLTRLDLSENQIQGIPRKAFRGVTGVKNLQLDNNHISCIE
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                                                                                                                                                                                                                             QRLPVREV---PFR-----
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                       growth factor-binding
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   (Norway

    3%; Score 346; DB 2; Length 1523;
    3%; Pred. No. 3e-15;
    75; Mismatches 226; Indels 142;

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                       protein
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C;Date: 30-Sep-1993 #sequence_revision Jursep-C;Accession: JC1282
R;Dai, J; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1
A;Title: Molecular cloning of the acid-labile
A;Reference number: JC1282; MUID:93038676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: liver
A;Note: the authors translated the codon AAG for residue 63 as Arg, AAA for resi
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-603/Product: insulin-like growth factor binding protein, acid labile chain
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
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A; Residues: 1-603 < DAI>
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Best Local Similarity
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 HFV-HC
                                  EMTDHC
                                                                  CSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPANVSGLDLRDVSET
                                                                                                       CDCVIR----WANATGTRVRFIEP--
                                                                                                                                       GPLQRAFWLDISHNHLETLAEGLFSSLGRVRYLSLRNNSLQTFSPQPGLERLWLDANPWD
                                                                                                                                                                                                        NSISSIEEQSLAGLSELLELDLTTN-RLTHLPRQLFQGLGHLEYLLLSYNQLTTLSAEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LANLTELDLSQNSFSDARDCDFHALPQLLSLHLEENQLTRLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALLG- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLAFWVALGPCHLQGTDPGASADAE----GPQCPVACTCS----
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Pred. No. 1e-15;
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le subunit
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insulin-like growth factor binding complex acid labile chain - m (;Species: Mus musculis (house mouse) C;Date: 23-Mar-1997 #sequence\_revision 09-May-1997 #text\_change C;Accession: JC6128

mouse

05-Nov-1999

JC6128

RESULT

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R;Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T. Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
A;Title: Organization and chromosomal localization of the gene encoding the A;Reference number: JC6128; MUID:96413591
A;Accession: JC6128
A;Accession: JC6128
A;Kolecule type: DNA
A;Residues: 1-603 <BOLY
A;Cross-references: GB:U66900; NID:g1621612; PIDN:AAB17270.1; PID:g1621613
C;Comment: This protein is a serum protein and it is of the ternary complex A;Map position: 17
RESULT 13
B36665
Slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster or;Date: 30-Apr-1991 #text_change 19-
C;Apte: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 19-
C;Accession: B36665
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, Genes Dev. 4, 2199-2187, 1990
A;Title: slit: an extracellular protein necessary for development characteristics.
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Pred. No. 1.3e-15;
9; Mismatches 190;
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                    development of midline glia
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F;1068-1099/Domain:
F;1115-1148/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: unassigned EGF-related proteins; EGF homology; leucine-rich alpha-2-gl F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1469 <R
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F;651-695/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;512-537/Domain:
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F;419-442/Domain:
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F;347-370/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;197-220/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F; 173-196/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;149-172/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;846-890/Domain:
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Best Local Similarity
Matches 103; Conser
835
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                                                 ESLPNLQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVP
                                                                                                                                                                                                                   CTGTVVACSRNQLKEIPR----GIPAETSELYLESNEIEQIHYERIRHLRSLTRLDLSN-
                                                                                                                                                                                                                                                                                                                             LAWFAECVRKKSLNGGAARCGAPSKVRDVQIKDLPHSEFKCSSENSEGCLGDGYCPPSCT
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EDLKSLTHIALGSNPLYCDCGLKWF-SDWIKLDYVEPGIARCAEPEQMKDKLILSTP
                                                                                                         NOITILSNYTFANLTKLSTLIISYN-KLQCLQRHALSGLNNLRVVSLHGNRISMLPEGSF
                                                                                                                                                        EELVSIDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTV 355
                                                                                                                                                                                                                                                                  -SLSFYDNQLARVPRRALEQVPG-LKFLDLNKNPLQRVGPGDFANMLHLKELGLNNM
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in: proteoglycan carboxyl-terminal homology <PCS1>
in: proteoglycan amino-terminal homology <PCS1>
in: leucine-rich alpha-2-glycoprotein repeat homology <LR
in: proteoglycan carboxyl-terminal homology <PCS2>
in: proteoglycan amino-terminal homology <PCS2>
in: leucine-rich alpha-2-glycoprotein repeat homology <LR
in: leucine-rich alpha-2-glycoprotein repeat homology <IR
in: proteoglycan carboxyl-terminal homology <PCS3>
in: proteoglycan carboxyl-terminal homo
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n: EGF homology <EGF>
n: EGF homology <EGF2>
n: EGF homology <EGF1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 324; DB 2
Pred. No. 9e-14;
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<LR10>
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  890
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RESULT A36665

Sat

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Cell 55, 1047-1059, 1988

A;Title: slit: An EGF-homologous locus of D. melanogaster i A;Reference number: A31640; MUID:89077533

A;Reference number: A31640; MUID:89077533

A;Reference number: A31640; MUID:89077533

A;Residues: 881-1182, 'G',1185-1404, 'GT',1463-1464, 'YHA' <RC A;Residues: 881-1182, 'G',1185-1404, 'GT',1463-1464, 'YHA' <RC A;Residues: 881-1182, 'G',1185-1404, 'GT',1463-1464, 'YHA' <RC A;Cross-references: GB:M23543; NID:g340939; PID:g514357

C;Genetics: A;Gene: FlyBase:sli
A;Gene: FlyBase:sli
A;Gross-references: FlyBase:FBgn0003425

A;Introns: 1351/3
A;Gross-references: FlyBase:FBgn0003425

A;Introns: 1351/3
A;Gross-references: FlyBase:rBgn0003425

A;Gross-references: FlyBase:rBgn0003425

A;Introns: 1351/3
A;Gross-references: FlyBase:rBgn0003425

A;Gross-references: FlyBase:rBgn0003425

A;Introns: 1351/3
A;Gross-references: FlyBase:rBgn0003425

A;Gross-references: FlyBase:
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A; Cross-references: GB: X53959; NID: g8614; R; Rothberg, J.M.; Hartley, D.A.; Walther,
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F;791-814/Domain:
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F;1115-1148/Domain:
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  GENKIKEISNKMFLGLHQLKTLNLYDNQISCVMPGSFEHLNSLTSLNLASNPFNC--NCH
                                                                                                                                            LGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHLEENQLTRLEDHSFAGLASLQELYL 148
                                                                                                                                                                                                                                                                           CPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAVPPALPAGTQTLLLQSNSIVRVDQSE 88
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                                                        NHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEMLPNLEILMIGGNKVDAILDMN 208
                                                                                                                                                                                                                        CPAMCHC--
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                                                                                                                                                                                                                                                                                                                                                               Similarity
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24.7%;
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alpha-2-glycoprotein repeat homology
alpha-2-glycoprotein repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <EGF2>
                                                                                                                                                                                                                                                                                                                                                                  Score 324; DB 2; Pred. No. 9.1e-14;
                                                                                                             FGRLPHLVKLELKRNQLTGIEPNAFEGASHIQELQL
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Z.; Artavanis-Tsakonas, S.
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A; Accession: A; Accession: A; Accession: A; Accession: B35483 A; Access
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A; Cross references: EMBL:Z23091; NID:g312501; PIDN:CAA80637.1;
R; Shimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda,
Blood 75, 2349-2356, 1990
A; Title: Rapid purification and characterization of human plate
A; Reference number: A60164; MUID:90275263
A; Accession: A60164
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A; Residues: 365-384, 'X',386-390, 'X',592-395, 'X',397;188-208, 'I',210;27-50, 'X',52-53;1
A; Residues: 365-284, 'X',386-390, 'X',56-57;'G',479-487, 'X',489-498, 'X',500, 'X',502-503, 'XX',108, 'T',61-72, 'TX',75-77;'V',56-57;'G',479-487, 'X',489-498, 'X',500, 'X',502-503, R; Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A.
Blochem, Blophys. Res. Commun. 170, 153-161, 190
A;Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related the A; Reference number: A35483; MUID:90321220
A; Accession: A35483
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C;Date: 12-Jan-1993 #sequence_revision
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                                                                                                                                                                             A;Molecule type: protein
A;Residues: 477-478, 'FX', 481-485, 'E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498
A;Residues: 477-478, 'FX', 481-485, 'E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498
R;Hickey, M.J.; Hagen, F.S.; Yaqi, M.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 193
A;Title: Human platelet glycoprotein V: characterization of the polypeptid A;Reference number: A47507; MUID:93391348
A;Accession: A47507
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A; Residues: 252-266, 'H', 268-272, 'X', 274-279, 'I', 281-284, 'I', 286
A; Residues: 152-266 the fragment was designated peptide M401
A; Note: this proteolytic fragment was designated peptide M401
R; Zafar, R.S.; Walz, D.A.
Thromb. Res. 53, 31-44, 1989
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A; Residues: 1-560 <L
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                                                                                    A; Status: preliminary; A; Molecule type: mRNA
                               A; Residues: 1-560 < RES>
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GB:L11238; NID:g388759;
                                                                                                                                              translated
                                                                                                                                              from GB/EMBL/DDBJ
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35483; C35483; A60432; A47507; S34329
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PIDN: AAA03069.1;
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PID:9388760
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K.; Fujimoto,
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C;Comment: The amino end of the intact protein is blocked.
C;Comment: This protein is absent in Bernard-Soulier syndrome.
C;Genetics:
A;Gene: GDB:GP5
A;Gene: GDB:GDB:230236; OMIM:173511
A;Map position: Spter-Sqter
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prot
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Search completed: August 31, 2002, 14:36:40 Job time: 102 sec
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                                                                                                       465
                                                                                                                                         411 VPFREMTDHCLPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIY-WVTP 460
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                                                                                                                                                                                                                           355 VESLPHLQEVGLHGNPIRCDC----VIRWANATGTRVRETEPQSTLCAEPPDLQRLPVRE 410
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                                                                                                       LPGGDA--EC---PGPRGPPPRPAADSSSEAPVH-PALAPNSSEPWVWAQP 509
                                                                                                                                                                                                                                                                        HSNGLTALPDGLLRGLGKLRQVSLRRNRLRALPRALFRNLSSLESVQLDHNQLETLPGDV 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLCAVLGLLRAQP-----FPCPPACKC------VFRDAAQCSGGDVARISAL--GL 48
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Title:
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No.
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Listing first 45 summaries
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          on:
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Gapop 10.0 , Gapext 0.5
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3732
1 MRLLVAPLLLAWVAGATATV......RKLPRSSEGETLLPPLSQNS
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        Length DB
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Q99mb1 mus musculu
008770 rattus norv
Q27972 bos taurus
P27792 homo sapien
015455 homo sapien
015455 homo sapien
015455 homo sapien
P82963 tribolium c
P82963 sus scrofa
P58661 mus musculu
09nr96 homo sapien
P82963 mus musculu
09nr96 homo sapien
P88654 mus musculu
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P08953
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equus cabal
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8 homo sapien
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## ALIGNMENTS

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FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVG
                                                            ILLSWYTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA
                                                                                                       TLELRRVTAEEAGLYTCVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYH
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LRR 2.

LRR 3.

LRR 4.

LRR 5.

LRR 6.

LRR 7.

LRR 7.

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LRR
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
EC8BC0FD240C9396 CRC66
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Interpro; IPR000483; LRR.
Interpro; IPR000372; LRR.
Interpro; IPR003592; LRR.
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Interpro; IPR003591; LRR.
Pfam; PF00560; LRR.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRUT; 1.
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01-JUN-1994 (
01-MAR-2002 (
Insulin-like
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P35858;
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                                                                                                                                                                                                                  use by non-profit institute modified and this statement entities requires a license
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Baxter R.C., Martin J.L., Beniac V.P.
"High molecular weight insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor (ALS).
IGFALS OR ALS.
                                                                                                                                                    EMBL; M86826; AAA36047.1; -. EMBL; AL031724; CAC36078.1; PJR; A41915; A41915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leong S.R., Baxter R.C., Camerato T., Dai J., Wood W.I.; 
"Structure and functional expression of the acid-labile su
the insulin-like growth factor-binding protein complex.";
Mol. Endocrinol. 6:870-876(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92357025; PubMed=1379671;
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                                                                                                                                                                                                                                                                                                                                               FUNCTION: INVOLVED IN PROTEIN-PROTEIN IN PROTEIN COMPLEXES, RECEPTOR-LIGAND SUBUNIT: FORMS A TERNARY COMPLEX OF ALL
                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 20 LEUCINE-RICH REPEATS (LRR).
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TISSUE SPECIFICITY: PLASMA.
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(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
e growth factor binding protein co
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Pred. No. 6.
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6.5e-22;
3s 173;
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SMART; SM00370; LRR; 2.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRRT; 1.
SMART; SM00013; LRR_TYP; 11
                                                                                                                                      Pfam; PF00560; LRR; 19
Pfam; PF01463; LRRCT;
Pfam; PF01462; LRRNT;
                                                                    Glycoprotein;
SIGNAL
                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        ALS_PAPHA STANDARD; PRT; 6
002833;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Insulin-like growth factor binding pro
                                                            CHAIN
                                                                                                                                                                                                                      EMBL; S83462; -; NC HSSP; P23945; 1XUN.
                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Papio.
NCBI_TaxID=9557;
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Eukaryota; Metazoa; Chordata; Craniata; V.
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor (ALS).
IGFALS OR ALS.
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IPR000483; LRR.
IPR000372; LRR.
IPR003592; LRR.
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LRR_typ.
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BY SIMILARITY.

INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN.
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i; Cercopithecidae;
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RDL
              REV
                            {\tt GNPWDCSCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPVYTYNNITCASPPEVAGLDL}
                                                                                     LNNMEELVSIDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSAL-
                                                                                                                                              LSHNAIASLRPRTFEDLHFLEELQLGHNRIRQLAERSFEGLGQLEVLTLDHNQLQEVKVG
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                                                         ADALGPLQRAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNNSLRTFTPQPPGLERLWLE
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Pred. No. 3.
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(POTENTIAL).
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ALS_RATION ALSO CONTROL OF ALS
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Interpro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 19.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
Pfan; PF01462; LRRNT; 1.
PRNUTS; PR00019; LEURICCHPPT.
SMART; SM00370; LRR; 5.
SMART; SM00018; LRRCT; 1.
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p35859;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Insulin-like growth factor binding pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dai J., Baxter R.C.;
Dai J., Baxter R.C.;
Wolecular cloning of the acid-labile subunit of to growth factor binding protein complex.";
sicchem. Blophys. Res. Commun. 188:304-309(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Purification and characterization of the serum insulin-like growth factor binding pendocrinology 134:848-852(1994).
-i- punction: MAY HAVE AN IMPORTANT ROLE I CIRCULATING IGFS TO THE TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Liver;
MEDLINE=93038676; PubMed=1384485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=WISTAR; TISSUE=Serum; MEDLINE=94130835; PubMed=7507839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 24-44, AND CHARACTERIZATION STRAIN-WISTAR; TISSUE-Serum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                      Glycoprotein; SIGNAL
                                                                                                                                                    CHAIN
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SUBUNIT: FORMS A TERNARY COMPLEX OF
IGF-I OR IGF-II AND IGFBP-3.
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: BRAIN, KIDNEY, L
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IPR000372;
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Rodentia;
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LRR 6.
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Sciurognathi;
                                                                                                                                   INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN.
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thi; Muridae;
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 HFV-HC
                                                    CSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPANVSGLDLRDVSET
                                                                                    CDCVIR-----WANATGTRVRFIEP-----
                                                                                                                                                                        NSISSIEEQSLAGLSELLELDLTIN-RLTHLPRQLFQGLGHLEYLLLSYNQLTTLSAEVL
                                                                                                                                                                                                                                     LFNVAVMNLSGNCLRSLPERVFQGLDKLHSLHLEHSCLGHVRLHTFAGLSGLRRLFLRD-
                                                                                                                                                                                                                                                                                              {\tt AIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEVLTLNDNQITEVRVGAFSG}
                                                                                                                                                                                                                                                                                                                                                         LPRLQKLYLDRNLITAVAPGAFLGMKALRWLDLSHNRVAGLMEDTFPGLLGLHVLRLAHN
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Pred. No. 2.6e
63; Mismatches
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ALS_MOUSE

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ALS_MOUSE

ALS_MOUSE

AC

P70389;

DT

O1-NOV-1997 (Rel. 35, Created)

DT

O1-NOV-1997 (Rel. 35, Last sequence update)

DR

Novelland (Novel)

RN

SIRAL SCOR ALS

O2 Nus musculus (Novel)

RN

SIRAL SCOR ALS

O2 Nus musculus (Novel)

RN

O1-SULLAN-1997 (Novel)

CC

O1-SUBULIT-PONE A TRANKT CONCLEX OF ABOUT 144

IGF-1 ON IGF-11 AND IGFED-3 (BY SIMILARITY)

CC

-1-SUBULIT-PONE A TRANKT CONCLEX OF ABOUT 144

IGF-1 ON IGF-11 AND IGFED-3 (BY SIMILARITY)

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-1-SUBULIT-PONE A TRANKT CONCLEX OF ABOUT 144

IGF-1 ON IGF-11 AND IGFED-3 (BY SIMILARITY)

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-1-SUBULIT-PONE A TRANKT CONCLEX OF ABOUT 144

IGF-1 ON IGF-11 AND IGFED-3 (BY SIMILARITY)

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IGF-1 ON IGF-11 AND IGFED-3 (BY SIMILARITY)

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IGF-1 ON IGF-11 AND IGFED-3 (BY SIMILARITY)

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-1-SUBULIT-PONE A TRANKT CONCLEX OF ABOUT 144

IGF-1 ON IGF-11 AND IGFED-3 (BY SIMILARITY)

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-1-SUBULIT-PO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIRCULATING IGFS TO THE TISSUES.

1. SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 15 IGF-1 OR IGF-II AND IGEBP-3 (BY SIMILARITY).

1. SUBCELLULAR LOCATION: Extracellular.

1. SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96413591; PubMed=8816745;
Boisclair Y.R., Seto D., Hsieh S., Hurst K.R., Ooi G.T.;
"Organization and chromosomal localization of the gene encoding
mouse acid labile subunit of the insulin-like growth factor bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cad. Sci. U.S.A. 93:10028-10033(1996).
MAY HAVE AN IMPORTANT ROLE IN REGULATING
NG IGFS TO THE TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                             repeat; Repeat; Signal.
BY SIMILARITY.
INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN COMPLEX ACID LABILE CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.isb-sib.ch/announce/
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409 433 458 482 505 543 64 85 96 368 515 578 603

REPEAT REPEAT REPEAT

Query Match Best Local S Matches 139

139;

CARBOHYD CARBOHYD SEQUENCE

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PV_MOUSE STANDARD
008742;
15-JUL-1998 (Rel. 36, C)
15-JUL-1998 (Rel. 36, L)
16-OCT-2001 (Rel. 40, L)
25 Platelet glycoprotein V
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                                                                                                                                                                                           EMTDHCLPLISPRSFPPSLQVASGESMVLHC |:: :||
                                                                                                                                                                                                                                                                          CDCVIR-----WANATGTRVRFIEP---
                                                                                                                                                                                                                                                                                                                                                                            NSISSIEEQSLAGLSELLELDLTAN-QLTHLPRQLFQGLGQLEYLLLSNNQLTMLSEDVL
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                                                                                                                                                                                                                                        {\tt CSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPANVSGLDLRDI---}
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   Created)
Last sequence update)
Last annotation updat
V precursor (GPV) (CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNM
   precursor (GPV) (CD42D).
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LRR 18.
LRR 19.
LRR 20.
LRR 20.
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        Ravanat C., Morales M., Azorsa D.O., Moog S., Schuhle Grunert P., Loew D., van Dorsselaer A., Cazenave J.F. "Gene Cloning of rat and mouse platelet glycoprotein identification of megakaryocyte-specific promoters an of functional thrombin cleavage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6; TJ
                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as lon-
modified and this statement is not remov-
entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97275136; PubMed=9129030;
                                                                                                                                            REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00560; LRR; 13. Pfam; PF01463; LRRCT; 1
                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 269595; CAA93441.1; -.
                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   functional thrombin cleavage.";

ood 89:3253-3262(1997).

FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND
FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT
PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO
INJURED VASCULAR SURFACES IN THE AFTERIAL CIRCULATION IS A
CRITICAL INITIATING EVENT IN HEMOSTASIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS; PR00019; LEURICHRPT.
[; SM00370; LRR; 1.
[; SM00082; LRRCT; 1.
[; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               SMOVOCIS; LRRN:, -
SM00369; LRR_TYP; 10.
SM00369; LRR_TYP; 10.
""ansmembrane; Glycoprotein; Blow
""ansmembrane; Cell adhesion;
"""ansmembrane; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000483;
IPR000372;
IPR003592;
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          194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRR_typ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRR_out.
            LERR 1.
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                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
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PLATELET GLYCOPROTEIN
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ave J.-P.,
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01-MAR-1992
01-MAR-2002
Slit protein
SLI.
                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tirsecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musccephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=91099665; PubMed=2176636;
Rothberg J.M., Jacobs J.R., Goodman C.S., Arta
"Slit: an extracellular protein necessary for
                                                                                                                                                glia and commissural axon
                                                                                                                                                                                                                                                                                                                                                                                                                         SLIT_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                          DROME
                                                                                                                                 domains.";
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SH
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXCRETED BY THE MIDLINE GLIA
EVENTUALLY DISTRIBUTED ALONG THE AXONS.
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                                                                    PS Dev. 4:2169-2187(1990).
FUNCTION: NECESSARY FOR DEVELOPMENT COMMISSURAL AXON PATHWAYS. SLIT MAY MATRIX MOLECULES.
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132; Conserv
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(Rel. 21, Last sequence update)
(Rel. 41, Last annotation update)
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Pred. No. 4.
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4.2e-17;
hes 217;
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   PRESENTATION OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00282; LamG; 1.

PROSITE; PS00010; ASX_HYDROXYL

PROSITE; PS01185; CTCK_1; 1.

PROSITE; PS01125; CTCK_2; 1.

PROSITE; PS00125; EGF_1; 7.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01187; EGF_CA; 2.

PROSITE; PS01187; EGF_CA; 2.

PROSITE; PS00125; LAM_G_DOMAIN

PROSITE; PS00125; LAM_G_DOMAIN

PROSITE; PS00125; LAM_G_DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00007; Cys_knot; 1.
Pfam; PF00008; EGF; 7.
Pfam; PF00054; Laminin_G; 1.
Pfam; PF000560; LRR; 17.
Pfam; PF00463; LRRCT; 4.
Pfam; PF01463; LRRCT; 4.
SMART; SM00041; CT; 1.
SMART; SM000179; EGF_CA; 2.
SMART; SM00001; EGF_Like; 5.
SMART; SM00001; LRR; 4.
SMART; SM000013; LRRCT; 4.
SMART; SM00013; LRRCT; 4.
SMART; SM00013; LRRCT; 4.
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InterPro; IPR000742; E
InterPro; IPR001881; E
InterPro; IPR001881; I
InterPro; IPR000483; I
InterPro; IPR000372; I
InterPro; IPR003592; I
InterPro; IPR003591; I
InterPro; IPR003791; I
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EGF-like doma:
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SIMILARITY: CONTAINS 24 LEUCHE-RICH REPAITS (LRR).
SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE
SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; A36665; I
;; P00743;
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IPR000359; Cys_knot.

IPR00051; EGF-like.

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; IPR001881; EGF_Ca.
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A36665.
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Glycoprotein; Signal; Alternatiin; Repeat; Leucine-rich repeat.
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01-FEB-1995
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16-OCT-2001
                                                                       Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94012616; PubMed=8407908; Lanza F., Morales M., de la Salle Shimomura T., Phillips D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Platelet;
MEDLINE=94012616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93391348; PubMed=769959;
Hickey M.J., Hagen F.S., Yagi M., Roth G.J.;
"Human platelet glycoprotein V: characterization of
and the related Ib-V-IX receptor system of adhesive,
                                                                                                                                                                                             glycoprotein V: the amino acid sequence contains repetitive modules as in glycoprotein Ib."; Blood 75:2349-2356(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycoproteins."
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MEDLINE=93391348;
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Mammalia; Eutheria;
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                                                                                              "Human platelet glycoprotein V: a surface related to adhesion.";
                                                                                                                            Roth
                                                                                                                                        MEDLINE=90321220;
                                                                                                                                                       PARTIAL SEQUENCE.
TISSUE=Platelet;
                                                                                                                                                                                                                                                     Fujimoto T.,
Kuramoto A.;
                                                                                                                                                                                                                                                                              Shimomura T.,
                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                  "Cloning and characterization of the gene encoding the human platelet glycoprotein V. A member of the leucine-rich glycoprotein family cleaved during thrombin induced platelet activation."; J. Biol. Chem. 268:20801-20807(1993).
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CHEM. BIOPHYS. Res. COMMUN. 170:153-161(1990).
FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A CRITICAL INITIATING EVENT IN HEMOSTASIS.
SUBCELLULAR LOCATION: Type I membrane protein.
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T.A., McMullen B.A.,
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Suzuki M., ]
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                                                                                                              Williams S.A.; ace leucine-rich glycoprotein
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ara-Tanaka K., Titani
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PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L11238;
Z23091;
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PF01463; LRRCT;
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an email to license@isb-sib.ch).
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IPR000372;
IPR003592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
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    57;
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  Mismatches
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W (IN REF. 3).
PGG (IN REF. 2).
I (IN REF. 3).
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                                                                                                                                                                                  (IN REF
             DB 1;
.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation;
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                        Length 560;
                                                                  CRC64;
  Indels
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                                                   SEQUENCE FROM N.A.

STRAIN-BALB/c x NIH; TISSUE-Macrophage;
Applequist S.E., Ljunggren H.G.;

"Molecular cloning of mouse Toll-like receptor 3 cDNA.";

"Molecular cloning of mouse Toll-like receptor 3 cDNA.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: participates in the innate immune response to ragents. May be involved in the recognition of ds-RNA. Act

MyD88 and TRAF6, leading to NF-kappa-B activation, cytok.

secretion and the inflammatory response (By similarity).

-!- SUBUNIT: Binds MyD88 via their respective TIR domains (B:
                    + +
                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                            099MB1; 091ZM4;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Toll-11ke receptor 3 precursor.
                                                                                                                                                                                                                                 Alexopoulou L., Holt A.C., Medzi
"Recognition of double-stranded
Toll-like receptor 3.",
Nature 413:732-738(2001).
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           PubMed=11607032;
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similarity).
SUBCELLULAR LOCATION: Type I membrane protein (B. TISSUE SPECIFICITY: Highly expressed in lung. Afintraperitoneal injection of lipopolysaccharide,
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SMART; SM00370; LRR; 10.
SMART; SM00082; LRRCT; 1.
SMART; SM000013; LRRCT; 1.
SMART; SM00369; LRR_TYP; 1.
SMART; SM00355; TIR; 1.
PROSITE; PS50104; TIR; 1.
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SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMIL
SIMILARITY: CONTAINS 1 TIR DOMAIN.
SIMILARITY: CONTAINS 22 LEUCINE-RICH REPEATS (LRR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF01463;
PF01582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; IPR001611; LRR.
5; IPR000483; LRR.Cterm.
6; IPR000372; LRR.Nterm.
7; IPR003592; LRR.out.
7; IPR003591; LRR.typ.
7; IPR000157; TIR.
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  Repeat;
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LRRNT; 1.
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TIR; 1.
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  Institute of Bioinformatics
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cine-rich repeat; Glycoprotein.
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

LRR 1.

LRR 3.

LRR 4.

LRR 5.

LRR 6.

LRR 7.

LRR 7.

LRR 7.

LRR 7.

LRR 9.

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LRR 10.

LRR 11.

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LRR 12.
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TOLL-LIKE RECEPTOR
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Best Local Similarity 23.4
Matches 118; Conservative
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CARBOHYD
CONFLICT
SEQUENCE
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    MEDLINE-97275136; PubMed-9129030; MEDLINE-97275136; PubMed-9129030; Manual C., Morales M., Azorsa D.O., Moog S., Schuhler S., Grunart C., Morales M., Azorsa D.O., Moog S., Schuhler S., Grunart P., Lowe D., van Dorsselber A., Cazenave J.-P., Lanza F.; "Gene cloning of rat and mouse platelet glycoprotein V: "dentification of megakaryocyte-specific promoters and demonstration of functional thrombin cleavage."; Blood 89:3253-3262(1997).

-I- FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND -I-FACTOR RECEPTOR AND MEDLATES VON WILLEBRAND FACTOR-DEPENDENT PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                     STRAIN=WISTAR; TISSUE=Liver;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Pred. No. 6.8e
58; Mismatches
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SMART; SM00370; LRR; 2.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS CRITICAL INITIATING EVENT IN HEMOSTASIS (BY SIMILARITY). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
                                                                                     LVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAV
RLTRNKISHLPRAILDKMVLLEQLFLDHNALRDLDQNLFQKLLNLRDLCLNQNQLSFLPA 163
                 DLSQNSFSDARDCDFHALPQLLSLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAP
                                  AELGLPTNLTHILLFRMDRGVLQSHSFSGMTVLQRLMLSDSHISAIDPGTFNDLVKLKTL
                                                                      MLRSVLLSAVLSLVGAQP-----FPCPKTCKCVVR-
                                                       PP-ALPAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00560; LRR; 14
PF01463; LRRCT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z69594; CAA93440.1; -.
                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003592; 1
                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001611; LRR.
IPR000483; LRR_Cterm.
                                                                                                                                                       338
362
387
51
181
181
243
298
312
385
385
                                                                                                           Conservative
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544
73
97
122
145
169
194
217
2217
241
266
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; LRRNT; 1.
; LRR_TYP; 10.
                                                                                                                                                              63344
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                                                                                                                                                      MW;
                                                                                                           62;
                                                                                                         Score 313.5;
Pred. No. 3.8e
2; Mismatches
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N-LINKED
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N-LINKED
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                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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PLATELET GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                      CA10708E0D03707F
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                                                   -TQTLLLQSNSIVRVDQSELGYLANLTEL
                                                                                                                                                             (GLCNAC.)
(GLCNAC.)
(GLCNAC.)
(GLCNAC.)
(GLCNAC.)
(GLCNAC.)
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                                                                                                         ; DB 1;
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es 226;
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                                                                      -DAVQCSGGSVAHI
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RESULT 11
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InterPro;
InterPro;
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997
01-NOV-1997
30-MAY-2000
                        EMBL; U08018; AAA21330.1; -.
                                                                                                                                                                 J. Biol. Chem.
                                                                                                                                                                                            related
                                                                                                                                                                                                                                  MEDLINE=95113864; PubMed=7814406;
                                                                                                                                                                                                                      Ни В.,
                                                                                                                                                                                                                                                TISSUE=Bone;
                                                                                                                                                                                                                                                                                      Neame P.J., Sommarin Y., Boynton R.E., Figh structure of a 38-kba leucine-rich isolated from bovine cartilage. F. J. Biol. Chem. 269:21547-21554(1994).
                                                                                                                                                                                                                                                                                                                              MEDLINE=94342341; PubMed=8063792; Neame P.J., Sommarin Y., Boynton
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Crania: Mammalia; Eutheria; Cetartiodactyla; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAD
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                                                                                                                                                                                                                                                                                                                                                           rissuE=Cartilage;
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Q27972;
                                                                                                                                                                              inhibitors.
                                                                                                                                                                                                         "Isolation
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASLTFWELLQGDQWCPSSRGLPPDPPTENALKAPDPTQRPNSSQSWAWVQLVARGES---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAFSGLSNLLRLHLNSNLLRAIDSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSL
                                                                                                                                                                                                      Coulson L., Moyer B., Price ion and molecular cloning of
                                                                                                                                                                                           in
            IPR001611;
                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Bovine).
                                                                                                                                                                                                                                                             25-55 AND
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(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
rin precursor (Cartilage leucine-rich
                                                                                                                                                              270:431-436(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457
                                                                                                                                                                                                                                                               77-97
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the cystatin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone
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IPR000483;

LRR\_Cterm

SQ PITTING TO SQ

Weerasinghe D.K.

tandem

ic peptides comparison

Euteleostomi;

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RESULT 12
CBP8_HUMAN
ID CBP8_H
AC P22792
DT 01-AUG
DT 01-AUG
DT 16-OCT
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Best Local
 CBP8_HUMAN
P22792;
01-AUG-1991
01-AUG-1991
16-OCT-2001
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CONFLICT
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                                                                                                              LPNLQEVGLHGNPIRCDCVI----RWANATGTRVRFIEPQSTLCAEPPDLQRLPVRE
                                                                                                                                                                                                           QLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANM-LHLKELGLNNMEELVSIDKF--
                                                                                                                                                                                                                                LVNLFILQLNNNKIRELRSGAFQGAKDLRWLYLSENSLSSLQPGALDDVENLAKFYLDRN
                                                                                                                                                                                                                                                  LPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDN
                                                                                                                                                                                                                                                                          QIREVAAGAFRGLKQLIYLYLSHNDIRVLRAGAFDDLTELTYLYLDHNKVTELPRGLLSP
                                                                                                                                                                                                                                                                                                                                          PAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHLEEN
                                                                                                                                                                                                                                                                                                                                                                                     LLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAVPPAL
                                                                                                                                              GAFLGVTTLKHVHLENN
                                                                                                                                                                                      QLSSYPSAALSKLRVVEELKLSHNPLKSIPDNAFQSFGRYLETLWLDN----TNLEKFSD
                                                                                                                                                                                                                                                                                               QLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEM
                                                                                                                                                                -ALVNLPELTKLDITNNPRLSFIHPRAFHHLP-----QMETLMLNNNALSALHQQTVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01462;
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SM00013; LRRNT; 1.
SM00369; LRR_TYP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103
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1127
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LRRNT; 1.
                                             STANDARD;
                                                                                                   NPWKCTCQLRGLRRWLEAKTSR-----PDAT-CASPAKFRGQHIRD
  19,
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  Last sequence update)
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CHONDROADHERIN.
CHONDROADHERIN, MINOR FORM.
10 X 24 AA LEUCINE-RICH TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C -> Y (IN REF. 2).
C -> W (IN REF. 2).
C -> H (IN REF. 2).
C -> L (IN REF. 2).
S -> R (IN REF. 2).
DA79DC98AD3DD1F8
                                              PRT;
                                                                                                                                             -RLHQLPSNFPFDSLETLTLTN
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No. 2.4
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                                                                                                                                                                                                                                                                                                                                                                                                                               361;
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                                                                                                                                                                                                                                                                                                                                                                                                            13;
     MEDLINE-90094386; PubMed-2378615;
Tan F., Weerasinghe D.K., Skidgel R.A., Tamei H., Kaul R.K., Roninson I.B., Schilling J.W., Erdoes E.G.;
"The deduced protein sequence of the human carboxypeptidase N molecular weight subunit reveals the presence of leucine-rich repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOCHEM. BIOPHYS. Res. COMMUN. 154:1323-1329(1988).
-!- FUNCTION: THE 83 kDa SUBUNIT BINDS AND STABILIZES THE CATALYTIC SUBUNIT AT 37 DEGREES CELSIUS AND KEEPS IT IN CIRCULATION. UNDER SOME CIRCUMSTANCES IT MAY BE AN ALLOSTERIC MODIFIER OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carboxypeptidase N 83 kDa
                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE.
MEDLINE=88309120; PubMed=3408501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
     REPEAT
                                                                                                                                                                                                                                   PIR; A34901;
MIM; 603104;
                                                                                                                                                                                                                                                        EMBL; J05158; AAA51921.1;
                                                                                                                                                                                                                                                                                                 use by non-profit institutions a modified and this statement is not
                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                                                                                                                                                                                                                                                                                                   between the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Amino acid sequence of the N-terminus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skidgel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 265:13-19(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                    REPEAT
                                                                                                                                                                    SMART; SM00369;
                                                                                                                                                                              SMART; SM00013; LRRNT;
                                                                                                                                                                                        Pfam; PF00560;
                                                                                                                                                                                                 InterPro; IPR001611;
InterPro; IPR000372;
InterPro; IPR003591;
                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                     PTM: O-GLYCOSYLATED IN THE SER/THR-RICH REGION (POTENTIAL), PTM: WHETHER OR NOT ANY CYS RESIDUES PARTICIPATE IN INTRACHA BONDS IS UNKNOWN, BUT THEY DO NOT FORM INTERCHAIN DISULFIDE WITH THE 50 KDA CAMALYTIC SUBUNIT.

DISEASE: A COMPLETE ABSENCE OF THE ENZYME IS NOT CONSIDERED DISEASE: A COMPLETE ABSENCE OF THE ENZYME IS NOT CONSIDERED
                                                                                                                                                                                                                                                                                                                                                                  DISEASE: A COMPLETE ABSENCE OF THE ENZYME IS NOT CO
COMPATIBLE WITH LIFE.
SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: TETRAME INACTIVE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            he active subunit of human plasma carboxypeptidase other carboxypeptidases.";
                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.A., Bennett C.D., Schilling J.W.,
                                                                                                                                                          Leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TETRAMER OF TWO CATALYTIC
                                                                                                                                                                                                                                               A34901.
                                                                                                                                                                                          LRR; 11.
                                                                                                                                                                      LRR_TYP;
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                                                                                                                                                                                                                                                                                         license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                               LRR_Nterm
                                                                                                                                                          repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain (Carboxypeptidase N regulatory
      Craniata; Vertebrata; Catarrhini; Hominidae;
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01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                  LT 13
                                                                                                                    "A fam:
Toll.";
                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98118556; PubMed=9435236;
ROCK F.L., Hardiman G., Timans J.C., Kastelein R.A.,
ROCK F.L., Hardiman receptors structurally related to
                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                        Toll-like receptor
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 agents. May be involved in the recognition of ds RNA MyD88 and TRAF6, leading to NF-kappa-B activation, cyt secretion and the inflammatory response (By similarity SUBUNIT: Binds MyD88 via their respective TIR domains similarity).

SUBCELLULAR LOCATION: Type I membrane protein (By similsSUE SPECIFICITY: Expressed at high level in placent
                                                                                         FUNCTION: Participates in
                                                                                                                                                                                                                                                                                                                                                                            SLSKNQLTTLPEASSTPTTTCSTWPCTVTPGSATAPGLPLQLAAAVHRSAPEHPDLLRCP
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                                                                                                                                                                                                                                                                                                                                                                                                                              GTFAHLSNLRSLMLSYNAITHLPAGIFRDLEELVKLYLGSNNLTALHPALFQNLSKLELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAFHHLPQMETLMLNNNA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNAITHLPLSIFASLGNLTFLSLQWNMLRVLPAGLFA--HTPCLVGLSLTHN-QLETVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNPLQRVGPGDFANMLHLKELGLN-NMEELVSIDKFALVNLPELTKLDITNNPRLSFIHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPQCACQIRPWYTPRSSYREATTVDCNDLFLTAVPPALPAGTQTLLLQSNSIVRVDQSEL
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06; Conservative
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation
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338
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                                                                                      in the innate immune response to microbial
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N-LINKED (GLC
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Pred.
                                                                                                   95:588-593(1998).
                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                     PRT;
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                                       -kappa-B activation, cytokine
response (By similarity).
respective TIR domains (By
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No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00019;
SMART; SM00370; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreas. Also detected in CD11c+ immature dendritic cells. Only expressed in dendritic cells and not in other leukocyt including monocyte precursors.

SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.

SIMILARITY: CONTAINS 1 TIR DOMAIN.

SIMILARITY: CONTAINS 22 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S; PR00019; LEURICHRPT.; SM00370; LRR; 5.; SM00370; LRRCT; 1.; SM00082; LRRCT; 1.; SM00013; LRRNT; 1.; SM00369; LRR_TYP; 2.; SM00255; TIR; 1.
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IPR003591; LRR_typ.
IPR000157; TIR.
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TIR; 1
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TOLL-LIKE RECEPTOR
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                                                                                                                  GARP protein precursor (Garpin) predominant).
GARP.
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           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE-94235567; PubMed-8180135;
MEDLINE-94235567; PubMed-8180135;
MEDLINE-94235567; PubMed-8180135;
MEDLINE-94235567; PubMed-8180135;
MEDLINE-94235567; PubMed-8180135;
MEDLINE-94235567; PubMed-8180135;
                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL MORPHOGENESIS. MEDIATES HOMOPHILIC CELLULAR ADHESION (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: EXTRACELLULAR SURFACE OF R-CELL PLASMA MEMBRANE (BY SIMILARITY).
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                                                                                                                                                                                                                                                        SMART; SM00370; LRR; 6.
SMART; SM00369; LRR_TYP; 14
Glycoprotein; Membrane; Repo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way the content is in the content in the content is in the content in the content is in the content in the content in the content is in the content in the content in the content is in the content in the con
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Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Tenebrionidae; Tribolium.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chaoptin (Photoreceptor cell-specific membrane
                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00019; LEURICHRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF322227; AAK01654.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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Pro; IPR003591; LRR_typ.
PF00560; LRR; 19.
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Job time: 263 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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; SM00013;	SMART: SM00370; LRR; 4. SMART: SM00082; LRRCT: 1.	; SM00408;	'; SM00060;	PF01462;	PF01463; LRRCT	PF00560;	0047; ig; 1.	IPR003591;	IPR003592;	IPR000372;		IPR001611;	IPR003006;	IPR003598;	InterPro; IPR003961; FN_III.	EMBL; AB040930; BAA96021.1;	:143-150(20	large proteins in vitro.";	genes.XVII.The complete sequences of 100 new cDNA clones from brain	s of unidentified h		MEDLINE=20277482; PubMed=10819331;	SEQUENCE FROM N.A.	[1]	D=9606;	Primates; Catarrhini; Hominidae;	ro -	Homo sapiens (Human).	KIAA1497.	OTEIN (FRAGMENT)	(TremBirel. 19, Last annotation	(TrEMBLrel, 15,	01-OCT-2000 (TremBLrel. 15, Created)	1;	Q9P231 PRELIMINARY; PRT; 730 AA.		LT 1

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Q61809; Q1-NOV-1996 (TIEMBLES. 01, C
01-NOV-1996 (TIEMBLES. 01, L
01-DEC-2001 (TIEMBLES. 19, L
LEUCINE-RICH-REPEAT PROTEIN.
LERN1 OR NLRR-1.
    STRAIN-OUTBRED (ICR MOUSE OUTBRED STRAIN); TISSUE-BRAIN; MEDLINE-96352541; PubMed-8717337; Taguchi A., Wanaka A., Mori T., Matsumoto K., Imai Y., T
                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                   SEQUENCE FROM N.A.
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QETSTALAAVMGSMFAVISLASIAV
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Sciurognathi; Muridae;
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Best Local S
Matches 331
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Pfam; PF00047; ig; 1.

Pfam; PF000560; LRR; 9

Pfam; PF001463; LRRCT; 1.

Pfam; PF01462; LRRNT; 1.

SMART; SM00060; FN3; 1.

SMART; SM00408; IGC2; 1.

SMART; SM000807; LRRCT; 1.

SMART; SM00081; LRRCT; 1.

SMART; SM00081; LRRUT; 1.

SMART; SM000869; LRRCTT; 1.

SMART; SM000869; LRRCTT; 1.
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InterPro;
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"Molecular cloning of novel leucine-rich repeat proteins expression in the developing mouse nervous system.";

Brain Res. Mol. Brain Res. 35:31-40(1996).

EMBL; D45913; BAA08341.1; -.

EMBL; D45913; BAA08341.1; -.

EMBL; D45913; BAA08341.1; -.
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566
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                                                                                   RFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQVASGESMVLHCRA
                                                                                                                                                                                                                                                                                                        PHITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTKTAAFALDISD
          QGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEA------
                                          RVATIKVNGTLL---
                                                              KTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTWSSAS-SLRG
                                                                                                                                RFMEPLSMFCAMPPEYRGQQVKEVLIQDSSEQCLPMISHDTFPNHLNMDIGTTLFLDCRA
                                                                                                                                                                                                                                                               NFRPLSNLRSLVLAGMYLTDVPGNALVGLDSLESLSFYDNKLIKVPQLALQKVPNLKFLD
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                                                                                                                                                                                                                                                                                                                             LNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEMLPNLEILMIGGNKVDAILDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; IPR003961; FN_III.
2; IPR003598; Ig_c2.
2; IPR003506; Ig_MHC.
2; IPR001611; LRR.
2; IPR000483; LRR_Cterm.
2; IPR000372; LRR_Nterm.
2; IPR0003592; LRR_Cut.
2; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain.
AA; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80548 MW;
                                          -DGAQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                      45.2%; Score 1687; DB 11; 52.8%; Pred. No. 2.9e-120; tive 109; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5073FB4801D08F58 CRC64;
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Best Local S
Matches 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01462; LRRUT; 1.
PRINTS; PRO0019; LEURICHRPT.
SMART; SM0040B; IGC2; 1.
SMART; SM00370; LRR; 4.
SMART; SM0001B; LRRUT; 1.
SMART; SM0001B; LRRUT; 1.
SMART; SM0001B; LRRUT; 1.
SMART; SM0001B; LRRUT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              043377 PRELIMINARY;
043377;
01-JUN-1998 (TrEMBLrel. C
01-JUN-1998 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel: 1
PROBABLE LEUCINE-RICH REF
RG118D07.1.
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InterPro;
InterPro;
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InterPro;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murray J., Langston Y., Clarke C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ
EMBL; AC004142; AAC02752.1; -.
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Homo sapiens (Human).
Chordata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Mammalia; Eutheria;
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                  317
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                                                                                                                                                                                                                         TATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAVPPALPAGTQTLLL
                                                         LEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLPELTKLD
                                                                                                                     GGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQLARVPRRA
               ITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIRCDCV
                                          LQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPDLRKIE
                                                                                                       GENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPHVA
                                                                                                                                                                LSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDALPNLEILMI
                                                                                                                                                                                                                                                                                     TTLVQAVDKKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLL
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                                                                                                                                                                                                                                                                                                                                                    333;
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                                                                                                                                                                                                                                                                                                                                                  Similarity 47.2
33; Conservative
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; IPR003598; Ig_c2.
; IPR003006; Ig_MHC.
; IPR001611; LRR.
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IPR000372; LRR_Nterm.
IPR003592; LRR_out.
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705
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AA; 79
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LRR; 9.
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 REPEAT
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06, Last sequence update)
19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                    109;
                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                 Score 1656.5; I
Pred. No. 6e-118
09; Mismatches 2
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Catarrhini;
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RESULT
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            Pfam; PI
PRINTS;
SMART; S
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SMART; S
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InterPro;
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InterPro;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 79.4 KDA PROTEIN (NEURONAL LEUCINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9H3W5;
Q9H3W5;
                                                                                                                                   Pfam;
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Mammalia; Eutheria;
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                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                               Hamano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                        ; PF01462; LR
TS; PR00019;
T; SM00060; F
T; SM00409; I
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                                                                                                                                                                                                                                                                                                  o S., Inuzuka H., Morohashi A., Ohira M., Nakagawara n neuronal leucine-rich repeat protein 3(NLRR-3)."; tted (MAY-2001) to the EMBL/GenBank/DDBJ databases. AL1442092; CAC09450.1; -. AB060967; BAB47184.1; -.
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                                                                                                     PF01463;
                                                                                                                   PF00560;
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                                                                                                                                                 PF00041;
            SM00408;
SM00370;
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IPR003591;
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IPR003006;
IPR001611;
IPR000483;
                                                                                                                                                                                                                                                                      IPR003961;
IPR003599;
                                                                                                                                                                                           IPR000372;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Boecher
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                    LRRCT; 1.
                                                                                                                   LRR;
                                                                                                                                   ig; 1
       FN3; 1.
IG; 1.
IGc2; 1
LRR; 4.
                                                                      LEURICHRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EATSCHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVGGRR-
                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                          Ig.
Ig_c2.
Ig_MHC.
LRR.
                                                                                                                                                             LRR_typ
                                                                                                                                                                                                                                                                                    FN_III
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                                                                                                                                                                                           LRR_Nterm.
                                                                                                                                                                                                            LRR_Cterm.
                                                                                                                                                                              LRR_out.
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                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                      Brandt P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mewes
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                                                                                                                                                                                                                                                                                                                                                                                                       H.W., Weil B.,
DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Homo.
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Best Local
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SMART; SM00369; LRR_TYP;
Hypothetical protein; Imm
SEQUENCE 708 AA; 79424
                                                                                                                                         Q9ESY6 PRELIMINARY; PRT; 707 AA. Q9ESY6; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence up 01-DEC-2001 (TrEMBLrel. 19, Last annotation NEURONAL LEUCINE-RICH REPEAT PROTEIN-3.
                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116; [1]
                                                                                                                          NLRR3.
                                                                                                                                                                                                                                                                                                                                                                                            661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAGLASIQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFEMLPNLEILMI
                                                                                                                                                                                                                                                                                                                                                                                            YVRNYLQKPTFALGELYPPLINLWEAGKEKSTSLKVKATVIGLPTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLISCL-----SPEMNCDGGHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KWTAFVKTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWYTPPNTVSTNL
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CIATNLVGADLKSVMIKVDGSFPQ---DNNGSLNIKIRDIQANSVLVSWKASSKILKSSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDALPNLEILMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTNNIAKIEYS-TDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEENKLTELPEKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRMMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNVE
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333; Conserv
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708 AA; 79424 MW; 24710478D6B124D1 CRC64;
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Pred. No. 6e-118;
9; Mismatches 217;
                                               Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                     update)
on update)
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                                                  Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                         691
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                                                       Rattus.
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Best Local Similarity 47.5
Matches 337; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0019; LEURCHRPT.
SMART; SM00060; FN3; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
SMART; SM00401; IG_11Ke; 1.
SMART; SM00410; IG_11Ke; 1.
SMART; SM00370; LRR; 7.
SMART; SM00037; LRRC; 1.
SMART; SM00086; LRRCT; 1.
SMART; SM00086; LRRNT; 1.
SMART; SM000369; LRRNT; 1.
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003500; Ig_like.
InterPro; IPR003500; Ig_MHC.
InterPro; IPR00311; LRR.
InterPro; IPR00311; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_ttyp.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin
SEQUENCE 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF291437;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the gene expression. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rukamachi K., Matsuoka Y., Kitanaka C., Kuchino Y.,
"Rat neuronal leucine-rich repeat protein-3: cloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21433505; PubMed=11549284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SPRAGUE-DAWLEY;
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 484
                       423
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LAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKE
                                                                                FYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDK
                                                                                                                                                                                                                                                    LEENQLIRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSR
                                                                                                                                                                                                                                                                                                                                               APLQIHVLLGLAITALVQAGDKKVDCPQLCTCEIRPWFTPRSIYMEASTVDCNDLGLLNF
                                                                                                                                                                                                                                                                                                                                                         APLLLAWVAG--ATATVPVVPWHYPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAV
LRRYTAEEAGLYTCVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILL
                      IAPESFPSILDVEADSYVSLHCRATAEPQPEIYWITPSGKRLLPNTLREKFYVHSEGTLD
                                 ISIHSNPIRCDCVIRWINMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPL
                                                                                                                                                             FYDNRLNKVPQVALQKAVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELVSIDS
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291437; AAG00604.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
AA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   79064 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   44.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRR_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                           112;
                                                                                                                                                                                                                                                                                                                                                                                        Score 1649.5; DB 11; Length Pred. No. 2.1e-117; [2; Mismatches 229; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  26A210F671EDA875 CRC64;
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Best Local S
Matches 328
                                                                                                                                                                                                                      PRINTS; PRO0019; LEURICHPPT.
SMART; SM00406; FN3; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00370; LRR; 4.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00013; LRRUT; 1.
SMART; SM00016; LRR_TYP; 1.
IMMUNOGIODULIN domain; Signal.
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NON_TER
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Mus musculus (Mouse).
Mus musculus (Mouse).
Thervota; Metazoa; Chordata;
Theria; Rodentia;
                                                                                                                                                         SEQUENCE
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MGD; 1
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"Cloning a
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01-MAY-1997 (TrEMBLrel. 03,
01-DEC-2001 (TrEMBLrel. 19,
LEUCINE-RICH REPEAT PROTEIN
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P97860;
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InterPro; IPR003591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                     328;
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PF01462; LRRNT; 1.
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PF00560; LRR; 10.
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                                                                                  Similarity
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; IPR003598; Ig_c2.
; IPR003006; Ig_MHC.
; IPR001611; LRR.
; IPR000483; LRR_Cterm.
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and expression of a novel gene for a protein with leucine-
eats in the developing mouse nervous system.";
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707
707
                                                                   Conservative
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Last annotation update)
PRECURSOR (FRAGMENT).
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Pred. No. 2.5e-1
1; Mismatches 1
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225;
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                       leucine-rich repeat protein ex nervous system.";
Gene 221:159-166(1998).
EMBL; AB014462; BAA28530.1;
Interpro; IPR003961; FN. III.
Interpro; IPR003598; Ig_c2.
Interpro; IPR003106; Ig_MHC.
Interpro; IPR001611; LRR.
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01-AUG-1998
01-AUG-1998
01-DEC-2001
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MEDLINE=99070063; PubMed=9852961;
Hayata T., Uochi T., Asashima M.;
"Molecular cloning of XNLRR-1, a Xenopus
"Molecular cloning of Trotein expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; i
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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InterPro;
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   IPR000483;
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(TrEMBLrel. 07, Last sequence u)
(TrEMBLrel. 19, Last annotation
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LRR_Cterm
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AC Q9
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Best Local Similarity
Matches 335; Conserv
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SMART; SM00060; FN3; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
Q9H8V1;
01-MAR-2001
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Pfam;
Pfam;
                                  Q9H8V1
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InterPro;
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SEQUENCE 718
                                                                                                               602
                                                                                                                                         601 FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLA 643
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PF00560; LRR; 9.
PF01463; LRRCT; 1.
PF01462; LRRNT; 1.
                                                                                                            GLHQQAQRACINVTTK-GTSYSLTVTDQETSAALAAVMGSLFA
                                                                                                                                                                         LVSWKVSSSVLASNIKWSSATMKIDNPHITYTARVPADVHEYNLTHLQPATEYEVCLTVS
                                                                                                                                                                                            LLSWVTPPNTVSTNLTWSSAS-SLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA
                                                                                                                                                                                                                                    LQIFNVQVEDSGRYTCVAQNSEGADTKVATLRVNGTLL----DGTQALRLYVQQAESSSV
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                                                                                                                                                                                                                                                                                                                                                                  RNAMENLPELTKLEATNNPKLSYIHRSAFRNVPTLESLMLNNNALNSVYRGTVESLPÄLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPANLSLDTQVLLLQSNNIGKTN-GELQRLVNLTELDLSQNNFTSIHDVGLSNLSQLTTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLTACQLLLGLLTSSLTDSSAPAN-ECPQLCVCEIRPWFTPQSTYREATTVDCNDLRLTK
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rPro; IPR003592; LR
rPro; IPR003591; LR
rPro; IPR003591; LR
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 (TrEMBLrel. 16,
                                PRELIMINARY;
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AA; 80035 MW;
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LRR_out.
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Pred. No. 1.4e
98; Mismatches
 Created)
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15;
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Q9NUU4
ID Q1
AC Q1
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Q9NUU4;
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InterPro;
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431
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Query Match
Best Local Similarity
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Pfam; PF00560; LRR; 1.
Pfam; PF01463; LRRCT; 1.
SMART; SM00060; FN3; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; LRRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ13211 FIS, CLONE NT2RP4000907, HIGHLY SIMILAR
LEUCINE-RICH-REPEAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                   344 NNALSALHQOTVESLPNLQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDL 403
                                                                                                                                                      NLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTKNAAFAVDISDQETSTALAAVMGSMFA
                                                                                                                                NITRLLQATEYWACLQVAFADAHTQLACVWARTKEA------TSCHRALGDRPG
                                                                                                                                                                                                                                                                                                      NNALNAIYQKTVESLPNLREISIHSNPLRCDCVIHWINSNKTNIRFMEPLSMFCAMPPEY
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   ;; Score 875.5; DB 4;
; Pred. No. 1.3e-58;
69; Mismatches 110;
PRT;
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273
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Best Local S
Matches 151
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SMART; SM00370; LRR; 2.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 1.
SMART; SM00369; LRR_TYP; 1.
NON_TER 273 273
SEQUENCE 273 AA; 30832 MW;
                                                                                                                                                                         O9D1TO PRELIMINARY; PKT; U14 GA.
O9D1TO;
O9D1TO;
O1-JUN-2001 (TrembLrel. 17, Created)
O1-JUN-2001 (TrembLrel. 17, Last sequence update)
O1-DEC-2001 (TrembLrel. 19, Last annotation update)
ADULT MALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED
CLONE: 4930471K13, FULL INSERT SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Kanehori K.;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
PLACE1006239 PROTEIN (FRAGMENT).
Homo sapiens (Human).
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                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                               NCBI_TaxID=10090;
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Pfam; PF01462; LRRNT;
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       SEQUENCE FROM N.A
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mes 151; Conserv
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IPR000372; LRR_Nterm.
IPR003592; LRR_out.
IPR003591; LRR_typ.
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EMBL/GenBank/DDBJ databases
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Pred. No. 1e-49;
9; Mismatches
                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B59F070A6D7D11FF CRC64;
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RMSI P. P. 184032563. BAB32403.1; -. RMSI, P. 1970. TPROSEON. TO TRANSPORT T
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Best Local S
Matches 173
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Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
SMARR; SM00409; IG; 1.
SMARR; SM00408; IGc2; 1.
SMARR; SM00410; IG_11ke; 1.
SMARR; SM00081; LRRCT; 1.
SMARR; SM00082; LRRCT; 1.
SMARR; SM000869; LRRCT; 1.
SMARR; SM000369; LRRCTYP; 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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LNLSYNPIGTIE----GSMLH-----
                                                     LDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLPELTKLDITNNPRLSF
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Ig_c2.
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Pred. No. 2.9e-29;
7; Mismatches 251;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:17422).
Homo sapiens (Human).
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC011057; AAH11057.1; -.
SEQUENCE 614 AA; 69145 MW; EFD967E3B716698D CRC64;
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SMART; SM00013; LRRNT; 1.
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Osada N., Hida M., Kusuda J., Tanuma R., Is
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from
libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 69.2 KDA PROTEIN.
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NCBI_TaxID=9541;
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                                                                                                                                                                                                                                                    Pro; IPR003591; PF00047; ig; 1
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IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003598;
  il protein; Immunoglobulin domain.
614 AA; 69187 MW; BA6C8BC7C993BE9A CRC64;
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LRR_out.
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Query Match
Best Local Similarity
Matches 160; Conserv

Conservative

; 68

13.18;

Score 490; DB 6; pred. No. 6.4e-29; 9; Mismatches 229;

Length 614; Indels

128;

Gaps

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RAA W W RAA N Y Y RAA Y Y Y RESULT.
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Ishibashi T., Kanehori K., Yosida M., Watanabe S., Kısano J.,

Hotuta T., Hiraoka S., Mırakawa K., Takiguchi S., Kısano J.,

Hotuta T., Hiraoka S., Mırakawa K., Takida M., Yamashita H., Chiba

Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Ishii S.,

Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,

Yamamoto J., Isono Y., Kawai Hio Y., Salto K., Nishikawa T.,

Yamamoto J., Nakamura Y., Sekine M., Kikuchi H., Kanda K
                                                                                                                                                                                                                                                                  09BZ20;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-BEC-2001 (TrEMBLrel. 19, Last annotation update)
BA43BB23.1 (NEURONAL LEUCINE-RICH REPEAT PROTEIN) (CDNA FLJ31810
CLONE NTZRIZ009289, WEAKLY SIMILAR TO CARBOXYPEPTIDASE N 83 KDA
CHAIN)
                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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                                                                                                                                     Submitted
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Best Local Similarity 27.0%;
Matches 140; Conservative
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SMART;
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Suzuki Y., Sugano S., Nagahari K., Masuho Y.,
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; AL353746; CAC22713.1; -.
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n; PF01462; LRRWY; 1.
NTS; PR00019; LEURICHRPT.
RT; SM00409; IG; 1.
RT; SM00408; IGC2; 1.
RT; SM00410; IG_like; 1.
RT; SM00410; IG_Like; 1.
RT; SM00013; LRRCT; 1.
RT; SM000369; LRRCT; 1.
RT; SM000369; LRRCTYP; 10.
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LGDGTLEIRFAQDQDSGMYVCIASNAAGNDTFTASLTV
                                                                                                                             I----SPRSFPPSLQ---VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRV
                                                                                                                                                                                                                                                                                 AGMESDLIRLQELHIVGAQLRTIEPHSFQGLRELRVLNVSQNLLETLEENVFSSPRALEV
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                                                                                           YFTCKKPKIREKKLQHLLVDEGQTVQLECSADGDPQPVISWVTPRRFITTKSNGRA-TV
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AA; 68
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Ig_c2.
Ig_like.
Ig_MHC.
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LRR_Nterm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 468.5; DB 4;
; Pred. No. 2.7e-27;
84; Mismatches 221;
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, Nagai K., I
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Isogai T.;
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RESULT 14 P70193 ID P70193

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Best Local Similarity
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Pfam; PF000463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRUT; 1.
SMART; SM00408; IGC2; 3.
SMART; SM000370; LRR, 6.
SMART; SM000371; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM000369; LRR. TYP; 4.
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01-FEB-1997 (TrEMBLrel. 0
01-FEB-1997 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLRel. 1
MEMBRANE GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CDNA cloning of a novel membrane glycoprotein that is expressed specifically in glial cells in the mouse brain LIG-1: A protein with leucine-rich repeats and immunoglobulin-like domains.";

J. Biol. Chem. 271:22522-22527(1996).
EMBL; D78572; BABA11416.1;
ISSP; P56276; ITLK.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
  366
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HNEISGTIEDTSGAFTGLDNLSKLTLFGN-KIKSVAKRAFSGLESLEHLNLGENAIRSVQ
                                                                                                 RNNISRLTDGAFWGLSKMHVLHLEYNSLVEVNSGSLYGLTALHQLHLSNNSISRIQRDGW
                                                                                                                          GNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQLARVPR---
                      NMEELVSID--KFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALH 351
                                                SFCQKLHELILSFNNLTRLDEESLAELSSLSILRLSHNAISHIAEGAFKGLKSLRVLDLD
                                                                                                                                                  GLSRSLLTLRLSKNRITQLPVKAFK-LPRLTQLDLNRNRIRLIEGLTFQGLDSLEVLRLQ
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                                                                                                                                                                                                     NKILSYDGSQLKSYLSLEVLDLSSNNITEIRSSCFPNGLRIRELNLASNRISILESGAFD
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                                                                                                                                                                                                                                                                                                                                                       169;
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; IPR000483;
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IPR003592;
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Rodentia;
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23.2%;
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LRR_out.
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Ig_MHC.
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19,
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                                                                       RALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLN
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                   Score 442; DB 11;
Pred. No. 6.9e-25;
6; Mismatches 255;
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                                                                                                                                                                                                                                                                                                                                                                                                                  A13D0866CE4C203D CRC64;
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424
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Pfam; PF01462; LRRNT; 1
Pfam; PF01462; LRRNT; 1
PRINTS; PR00019; LEURIC
SMART; SM00409; IG; 1.
SMART; SM00408; IGc2; 1
SMART; SM00410; IG_11ke
SMART; SM00370; LRR; 6.
                                SMART;
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InterPro;
InterPro;
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                           Pfam; PF00047; ig; Pfam; PF00560; LRR;
                                                                                                                                                                                                                                                                                     XVIII. The complete sequences of 100 new cDNA clones from code for large proteins in vitro."; DNA Res. 7:273-281(2000).
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          Immunoglobulin
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Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human
                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                 SM00369;
                                          SM00013;
                                                       SM00082;
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IPR003006;
IPR001611;
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IPR000372;
640
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                                                               IG; 1.
; IGc2; 1.
; IG_like; 1.
LRR; 6.
AA;
                     domain
                                         LRRCT; 1.
LRRNT; 1.
                                LRR_TYP;
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71949
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Ig_like.
Ig_MHC.
LRR.
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WW;
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